



PT New antigens from Mycobacterium tuberculosis useful in diagnostic  
 PT skin tests and protective or therapeutic vaccines or compositions  
 XX  
 PS Example 5; Page 246; 239pp; English.

CC The present invention describes polypeptides comprising an immunogenic  
 CC part of a Mycobacterium tuberculosis antigen (Ag). Also described  
 CC are vaccines and fusion protein containing M. tuberculosis Ag's.  
 CC M. tuberculosis Ag's, DNAs encoding them, derived fusion proteins and  
 CC other polypeptides fragments, can be used in pharmaceutical compositions  
 CC or vaccines to generate a protective or therapeutic immune response to  
 CC M. tuberculosis and as reagents in skin tests for diagnosis of  
 CC tuberculosis. Ag can induce proliferation of, or cytokine secretion  
 CC by, T, B or natural killer cells and/or macrophages in  
 CC tuberculosis-immune subjects. AA219249 to AA219460 and AA219083 to  
 CC AA219225 are used in the exemplification of the present invention.

SQ Sequence 178 AA;

Query Match 17.8%; Score 28; DB 20; Length 178;

Best Local Similarity 30.8%; Pred. No. 1.8e+03;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Oy 17 PXXXXXXCXGXC 29

Db 103 PAAAAAQLCRGSC 115

RESULT 2

AA219075  
 ID AA219075 standard; Protein; 178 AA.

XX AAY39075;

DT 05-NOV-1999 (first entry)

XX M. tuberculosis recombinant antigen protein MO-39.

KW Antigen; diagnosis; detection; infection; antibody; immunisation;  
 KW vaccine; immunity.

OS Mycobacterium tuberculosis.

PN WO9942118-A2.

XX 26-AUG-1999.

PF 17-FEB-1999; 99WO-US03265.

PR 05-MAY-1998; 98US-0072596.

PR 18-FEB-1998; 98US-0024753.

PA (CORI-) CORIXA CORP.

PI Campos-Neto A, Dillon DC, Hendrickson RC, Houghton R;  
 PI Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR, Vedvick TS;

DR WPI; 1999-527416/44.

DR N-PSDB; AA219202.

XX New polypeptide comprising antigenic portions of M. tuberculosis

PS Example 5; Page 291; 323pp; English.

CC This invention describes novel recombinant antigens and their encoding  
 CC nucleic acids derived from Mycobacterium tuberculosis. The novel  
 CC polypeptides are useful for detecting M. tuberculosis infection in a  
 CC biological sample by detecting antibodies which bind with the  
 CC polypeptides, and are useful as vaccines for immunizing against  
 CC M. tuberculosis infection. The new detection methods are needed as  
 CC current vaccination strategies do not provide 100% immunity.

SQ Sequence 178 AA;

Query Match 17.8%; Score 28; DB 20; Length 178;  
 Best Local Similarity 30.8%; Pred. No. 1.8e+03;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Oy 17 PXXXXXXCXGXC 29

Db 103 PAAAAAQLCRGSC 115

RESULT 3

AA210118  
 ID AA210118 standard; Protein; 45 AA.

XX AA210118;

DT 06-NOV-2001 (first entry)

XX Human polypeptide SEQ ID NO 24010.

KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;

KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
 KW nervous system disorders; arthritis; inflammation.

OS Homo sapiens.

PN WO200164835-A2.

XX 07-SEP-2001.

PF 26-FEB-2001; 2001WO-US04927.

PR 28-FEB-2000; 2000US-0515126.

PR 18-MAY-2000; 2000US-0577409.

PA (HYSE-) HYSEQ INC.

PI Tang YF, Liu C, Drmanac RT;

DR WPI; 2001-514838/56.

DR N-PSDB; AA190049.

XX Isolated nucleic acids and polypeptides, useful for preventing  
 XX diagnosing and treating e.g. leukaemia, inflammation and immune  
 XX disorders -

PS Claim 20; SEQ ID NO 24010; 1399pp + Sequence Listing; English.

CC The invention relates to human polynucleotides (AA179941-AA193841) and  
 CC the encoded proteins (AA000010-AA013910) that exhibit activity elating to  
 CC cytokine, cell proliferation or cell differentiation or which may induce  
 CC production of other cytokines in other cell populations. The  
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
 CC peptide therapy. The polypeptides have various cytokine-like activities,  
 CC e.g. stem cell growth factor activity, haematopoiesis regulating  
 CC activity, tissue growth factor activity, immunomodulatory activity and  
 CC activin/inhibin activity and may be useful in the diagnosis and/or  
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
 CC inflammation.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

SQ Sequence 45 AA;

Query Match 17.2%; Score 27; DB 22; Length 45;

Best Local Similarity 30.8%; Pred. No. 1.1e+03;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Oy 17 PXXXXXXCXGXC 29

Db 28 PASASQAQCCGTC 40

RESULT 4  
AAB24498  
ID AAB24498 standard; Protein: 58 AA.  
XX  
AC AAB24498;  
XX  
DT 20-NOV-2000 (first entry)  
XX  
DE Human secreted protein sequence encoded by gene 7 SEQ ID NO:124.  
KW Human; secreted protein; cytostatic; antianaemic; antidiabetic;  
KW antinflammatory; ophthalmological; antirheumatic; antidiabetic;  
KW antipsoriatic; angiogenic; cardiac; anti-HIV; neutrotropic;  
KW neutrotropic; antimicrobial; antiparkinsonian; cancer;  
KW immune system disorder; angiogenesis; hyperproliferative disorder;  
KW cardiovascular disorder; apoptosis; neurological disease;  
KW infectious disease; wound healing.  
XX  
OS Homo sapiens.  
XX  
PN MO200035937-A1.  
XX  
PD 22-JUN-2000.  
XX  
PF 16-DEC-1999; 99WO-US29950.  
XX  
PR 17-DEC-1998; 98US-0112809.  
PR 18-DEC-1998; 98US-0113006.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
PI Ruben SM, Ebner R, Rosen CA, Endress GA, Soppet DR, Ni J;  
PI Duan DR, Moore PA, Shi Y, Lafleur DW, Olsen HS, Florence K;  
XX  
DR WPI: 2000-431566/37.  
XX  
PT Forty seven human nucleic acids encoding secreted proteins, useful in  
PT the treatment, prevention and diagnosis of cancers, disorders of the  
PT immune system, angiogenesis disorders, neurological diseases and  
PT hyperproliferative disorders -  
XX  
PS Disclosure: Page 26; 562pp; English.  
XX  
CC The polynucleotide sequence given in AAA78381 to AAA78432 encode the  
CC human secreted proteins given in AAB24437 to AAB24604. Human secreted  
CC proteins have activities based on the tissues and cells the genes are  
CC expressed in. Examples of activities include: cytostatic; antianaemic;  
CC antidiabetic; antinflammatory; ophthalmological; antirheumatic;  
CC antidiabetic; antipsoriatic; angiogenic; cardiac; anti-HIV;  
CC neutrotropic; neutrotropic; antimicrobial and antiparkinsonian.  
CC Human secreted protein polynucleotides, polypeptides, antagonists and/or  
CC agonists may be useful in treating, preventing, and/or diagnosing other  
CC diseases, disorders, and/or conditions such as: (a) cancers; (b)  
CC disorders of the immune system; (c) angiogenesis disorders; (d)  
CC hyperproliferative disorders; (e) cardiovascular disorders; (f) diseases  
CC associated with increase apoptosis; (g) neurological diseases; and  
CC (h) infectious diseases. They are also used to promote wound healing.  
CC AAA78377 to AAA78380 and AAB24436 represent sequences used in the  
CC exemplification of the present invention.  
XX  
SQ Sequence 58 AA;  
XX  
Query Match 17.2%; Score 27; DB 21; Length 58;  
Best Local Similarity 30.8%; Pred. No. 1.3e+03;  
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
OY 17 PXXXXXXCXCXC 29  
DB 8 PGAAAGACGAC 20

RESULT 5  
ABG05086  
ID ABG05086 standard; Protein: 125 AA.  
XX  
AC ABG05086;  
XX  
DT 13-FEB-2002 (first entry)  
XX  
DE Novel human diagnostic protein #5077.  
XX  
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200175067-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 30-MAR-2001; 2001WO-US08631.  
XX  
PR 31-MAR-2000; 2000US-0540217.  
PR 23-AUG-2000; 2000US-0649167.  
XX  
PA (HXSE-) HXSEQ INC.  
XX  
PI Drmanac RT, Liu C, Tang YT;  
XX  
DR WPI: 2001-639362/73.  
DR N-PSDB; AAS69273.  
XX  
PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity -  
XX  
PS Claim 20; SEQ ID NO 35445; 103pp; English.  
XX  
CC The invention relates to isolated polynucleotide (I) and  
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
CC and gene mapping, and in recombinant production of (II). The  
CC polynucleotides are also used in diagnostics as expressed sequence tags  
CC for identifying expressed genes. (I) is useful in gene therapy techniques  
CC to restore normal activity of (II) or to treat disease states involving  
CC (II). (II) is useful for generating antibodies against it, detecting or  
CC quantitating a polypeptide in tissue, as molecular weight markers and as  
CC a food supplement. (II) and its binding partners are useful in medical  
CC imaging of sites expressing (II). (I) and (II) are useful for treating  
CC disorders involving aberrant protein expression or biological activity.  
CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG00010-ABG30377 represent novel human  
CC diagnostic amino acid sequences of the invention.  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 125 AA;  
XX  
Query Match 17.2%; Score 27; DB 22; Length 125;  
Best Local Similarity 30.8%; Pred. No. 2.1e+03;  
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
OY 17 PXXXXXXCXCXC 29  
DB 13 PGALLSACSGAC 25

RESULT 6  
AAU19418

ID AAU19418 standard; Protein; 274 AA.  
 AC AAU19418;  
 XX  
 DT 04-DEC-2001 (first entry)  
 XX  
 DE Human diagnostic and therapeutic polypeptide (DITHP) #4.  
 XX  
 KW Human; receptor; diagnostic; therapeutic; gene therapy; vaccine;  
 KW cell proliferative disorder; Crohn's disease; lymphoma; leukemia;  
 KW acquired immune deficiency syndrome; AIDS; autoimmune disorder;  
 KW respiratory disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200162927-A2.  
 XX  
 PD 30-AUG-2001.  
 XX  
 PF 21-FEB-2001; 2001WO-US06059.  
 XX  
 PR 24-FEB-2000; 2000US-0184693.  
 PR 24-FEB-2000; 2000US-0184697.  
 PR 24-FEB-2000; 2000US-0184698.  
 PR 24-FEB-2000; 2000US-0184768.  
 PR 24-FEB-2000; 2000US-0184769.  
 PR 24-FEB-2000; 2000US-0184770.  
 PR 24-FEB-2000; 2000US-0184771.  
 PR 24-FEB-2000; 2000US-0184772.  
 PR 24-FEB-2000; 2000US-0184773.  
 PR 24-FEB-2000; 2000US-0184774.  
 PR 24-FEB-2000; 2000US-0184776.  
 PR 24-FEB-2000; 2000US-0184777.  
 PR 24-FEB-2000; 2000US-0184797.  
 PR 24-FEB-2000; 2000US-0184813.  
 PR 24-FEB-2000; 2000US-0184837.  
 PR 24-FEB-2000; 2000US-0184841.  
 PR 24-FEB-2000; 2000US-0185213.  
 PR 24-FEB-2000; 2000US-0185216.  
 PR 12-MAY-2000; 2000US-0203785.  
 PR 15-MAY-2000; 2000US-0204226.  
 PR 16-MAY-2000; 2000US-0204525.  
 PR 16-MAY-2000; 2000US-0204821.  
 PR 16-MAY-2000; 2000US-0204908.  
 PR 16-MAY-2000; 2000US-0205232.  
 PR 17-MAY-2000; 2000US-0204815.  
 PR 17-MAY-2000; 2000US-0204863.  
 PR 17-MAY-2000; 2000US-0205221.  
 PR 17-MAY-2000; 2000US-0205285.  
 PR 17-MAY-2000; 2000US-0205286.  
 PR 17-MAY-2000; 2000US-0205287.  
 PR 17-MAY-2000; 2000US-0205323.  
 PR 17-MAY-2000; 2000US-0205324.  
 XX  
 PA (INCYTE GENOMICS INC.  
 XX  
 PI Panzer SR, Spiro PA, Banville SC, Shah P, Chalup MS, Chang SC;  
 PI Chen A, D'Sa SA, Amshey S, Dahl CR, Dam TC, Daniels SE;  
 PI Dufour GE, Flores V, Fong WT, Greenawalt LB, Hillman JL, Jones AL;  
 PI Liu TF, Roseberry AM, Rosen BH, Russo PD, Stocktreher TK, Daffo A;  
 PI Wright RJ, Yap PE, Yu JY, Bradley DL, Bracher SR, Chen W;  
 PI Cohen HJ, Hodgson DM, Lincoln SE, Jackson S;  
 XX  
 DR WPI: 2001-502867/55.  
 DR N-PSDB: AAS30989.  
 XX  
 PT Polynucleotides encoding diagnostic and therapeutic proteins, e.g.  
 PT enzymes, hormones and receptors, useful in diagnostics and therapeutics  
 XX  
 PS Claim 27; Page 399-400; 522pp; English.  
 XX  
 CC The invention relates to polynucleotides (I) encoding diagnostic and

CC therapeutic (DITHP) polypeptides (II), which include e.g. enzymes,  
 CC and proteins involved in growth and development and receptors. (I) and  
 CC (II) may be used in the prevention, diagnosis and treatment of diseases  
 CC associated with inappropriate DITHP expression. For example, (I) and  
 CC (II) may be used to treat disorders associated with decreased polypeptide  
 CC expression by rectifying mutations or deletions in a patient's genome,  
 CC that affect the activity of the DITHPs, by expressing inactive proteins  
 CC or supplementing the patient's own production of them. (I) and (II)  
 CC may be used to treat diseases, for example, cell proliferative disorder,  
 CC Crohn's disease, acquired immune deficiency syndrome (AIDS), lymphoma,  
 CC leukemia, autoimmune disorders, and respiratory disorders. Additionally,  
 CC (I) may be used to produce the DITHPs, by inserting the nucleic acids  
 CC into a host cell and culturing the cell to express the protein. (I) and  
 CC its complementary sequences may also be used as DNA probes in diagnostic  
 CC assays to detect and quantitate the presence of similar nucleic acids in  
 CC samples, and therefore which patients may be in need of restorative  
 CC therapy. (II) may also be used as antigens in the production of  
 CC antibodies against DITHPs and in assays to identify modulators of DITHP  
 CC expression and activity. The anti-DITHP antibodies and antagonists may  
 CC also be used to down regulate expression and activity. The anti-DITHP  
 CC antibodies may also be used as diagnostic agents for detecting the  
 CC presence of DITHPs in samples (e.g. by enzyme linked immunosorbent  
 CC assay (ELISA)). AAU19415-AAU19625 represent human diagnostic and  
 CC therapeutic (DITHP) polypeptides of the invention.  
 XX  
 SQ Sequence 274 AA;  
 XX  
 Query Match 17.2%; Score 27; DB 22; Length 274;  
 Best Local Similarity 30.8%; Pred. No. 3.4e+03;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 QY 17 PXXXXXXCXCXC 29  
 Db 262 PCGSSSATCGSHC 274  
 XX  
 RESULT 7  
 AAB24499  
 ID AAB24499 standard; Protein; 468 AA.  
 XX  
 AC AAB24499;  
 XX  
 DT 20-NOV-2000 (first entry)  
 XX  
 DE Human secreted protein sequence encoded by gene 7 SEQ ID NO:125.  
 XX  
 KW Human; secreted protein; cytosolic; antianemic; antidiabetic;  
 KW antiinflammatory; ophthalmological; antirheumatic; antiarthritic;  
 KW antisoriatric; antiangiogenic; cardiant; anti-HIV; noctropic;  
 KW neuroprotective; antimicrobial; antiparkinsonian; cancer;  
 KW immune system disorder; angiogenesis; hyperproliferative disorder;  
 KW cardiovascular disorder; apoptosis; neurological disease;  
 KW infectious disease; wound healing.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200035937-A1.  
 XX  
 PD 22-JUN-2000.  
 XX  
 PF 16-DEC-1999; 99WO-US29950.  
 XX  
 PR 17-DEC-1998; 98US-0112809.  
 PR 18-DEC-1998; 98US-0113006.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Ruben SM, Ebner R, Rosen CA, Endress GA, Soppet DR, Ni J;  
 PI Duan DR, Moore PA, Shi Y, Lafleur DM, Olsen HS, Florence K;  
 XX  
 DR WPI: 2000-431566/37.  
 XX  
 PT Forty seven human nucleic acids encoding secreted proteins, useful in

PT the treatment, prevention and diagnosis of cancers, disorders of the  
PT immune system, angiogenesis disorders, neurological diseases and  
PT hyperproliferative disorders -

PS Disclosure: Page 25-26; 562pp; English.

CC The polynucleotide sequence given in AAB78381 to AAB78432 encode the  
CC human secreted proteins given in AAB24437 to AAB24604. Human secreted  
CC proteins have activities based on the tissues and cells the genes are  
CC expressed in. Examples of activities include: cytostatic; antineoplastic;  
CC antidiabetic; antiinflammatory; ophthalmological; antirheumatic;  
CC antiallergic; antiparasitic; antitumor; cardiant; anti-HIV;  
CC neurotrophic; neuroprotective; antimicrobial and antiparkinsonian.  
CC Human secreted protein polynucleotides, polypeptides, antagonists and/or  
CC agonists may be useful in treating, preventing, and/or diagnosing other  
CC diseases, disorders, and/or conditions such as: (a) cancers; (b)  
CC disorders of the immune system; (c) angiogenesis disorders; (d)  
CC hyperproliferative disorders; (e) cardiovascular disorders; (f) diseases  
CC associated with increase apoptosis; (g) neurological diseases; and  
CC (h) infectious diseases. They are also used to promote wound healing.  
CC AAB78372 to AAB78380 and AAB24436 represent sequences used in the  
CC exemplification of the present invention.

XX Sequence 468 AA;

Query Match 17.2%; Score 27; DB 21; Length 468;

Best Local Similarity 30.8%; Pred. No. 4.8e+03;

Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 17 PXXXXXXCXCXC 29

DB 8 PGAAAGACAGAC 20

RESULT 8  
AAB39643  
ID ABB39643 standard; Peptide: 59 AA.

XX ABB39643;

DT 04-FEB-2002 (first entry)

DE Peptide #7149 encoded by human foetal liver single exon probe.

KW Human; foetal liver; gene expression; single exon nucleic acid probe.

OS Homo sapiens.

PN WO200157277-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00669.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-483447/52.

XX Human genome-derived single exon nucleic acid probes useful for  
XX analyzing gene expression in human fetal liver -  
XX Claim 27; SEQ ID NO 32276; 639pp + sequence listing; English.

CC The invention relates to a single exon nucleic acid probe for  
CC measuring human gene expression in a sample derived from human foetal  
CC liver. The single exon nucleic acid probes may be used for predicting,  
CC measuring and displaying gene expression in samples derived from human  
CC fetal liver. The present sequence is a peptide encoded by a single exon  
CC nucleic acid probe of the invention.

CC Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp://ipoint.int/pub/published\_pct\_sequences.

XX Sequence 59 AA;

Query Match 16.6%; Score 26; DB 22; Length 59;

Best Local Similarity 30.8%; Pred. No. 1.8e+03;

Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 17 PXXXXXXCXCXC 29

DB 20 PGSSPPSACAGAC 32

RESULT 9  
AAB24324  
ID ABB24324 standard; Protein: 59 AA.

XX ABB24324;

DT 23-JAN-2002 (first entry)

DE Protein #6323 encoded by probe for measuring heart cell gene expression.

KW Human; gene expression; heart; microarray; vascular system;

KW cardiovascular disease; hypertension; cardiac arrhythmia;

KW congenital heart disease.

OS Homo sapiens.

PN WO200157274-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00666.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-488899/53.

XX Single exon nucleic acid probes for analyzing gene expression in human  
XX hearts -  
XX Claim 15; SEQ ID NO 26094; 530pp; English.

CC The present invention relates to single exon nucleic acid probes for  
CC measuring human gene expression in a sample derived from human heart (see  
CC ABA21535-ABA41305). The present sequence is a protein encoded by one such  
CC probe. The probes may be used for predicting, measuring and displaying  
CC gene expression in samples derived from the human heart via microarrays.  
CC By measuring gene expression, the probes are useful for predicting,  
CC diagnosing, grading, staging, monitoring and prognosing diseases of the  
CC human heart and vascular system e.g. cardiovascular disease,  
CC hypertension, cardiac arrhythmias and congenital heart disease.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published\_pcf\_sequences.

XX Sequence 59 AA;

Query Match 16.6%; Score 26; DB 22; Length 59;

Best Local Similarity 30.8%; Pred. No. 1.8e+03;

Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 17 PXXXXXXCXGXC 29

DB 20 PGSSPPSACAGAC 32

RESULT 10

AAM60355

ID AAM60355 standard; Protein: 59 AA.

AC AAM60355;

DT 05-NOV-2001 (first entry)

DE Human brain expressed single exon probe encoded protein SEQ ID NO: 32460.

XX Human: brain expressed exon; gene expression analysis; probe;

KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;

KW epilepsy; cancer.

XX Homo sapiens.

OS MO200157275-A2.

PN 09-AUG-2001.

PD 30-JAN-2001; 2001WO-US00667.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PA Penn SG, Hanzel DK, Chen W, Rank DR;

PI WPI; 2001-483446/52.

DR Single exon nucleic acid probes for analyzing gene expression in human

XX brains -

PT Example 4; SEQ ID NO: 32460; 650pp + Sequence Listing; English.

PS The present invention provides a number of single exon nucleic acid

XX probes which are derived from genomic sequences expressed in the human

CC brain. They can be used to measure gene expression in brain cell samples,

CC which may enable the diagnosis and improved treatment of nervous system

CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,

CC epilepsy and cancers. The present sequence is a protein encoded by one of

CC the probes of the invention.

XX Sequence 59 AA;

Query Match 16.6%; Score 26; DB 22; Length 59;

Best Local Similarity 30.8%; Pred. No. 1.8e+03;

Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 17 PXXXXXXCXGXC 29

DB 20 PGSSPPSACAGAC 32

RESULT 11

AAM72991

ID AAM72991 standard; Protein: 59 AA.

AC AAM72991;

DT 06-NOV-2001 (first entry)

DE Human bone marrow expressed probe encoded protein SEQ ID NO: 33297.

XX Human: bone marrow expressed exon; gene expression analysis; probe;

KW microarray; cancer; leukaemia; lymphoma; myeloma.

XX Homo sapiens.

OS MO200157276-A2.

PN 09-AUG-2001.

PD 30-JAN-2001; 2001WO-US00668.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PA Penn SG, Hanzel DK, Chen W, Rank DR;

PI WPI; 2001-488900/53.

DR Human genome-derived single exon nucleic acid probes useful for

XX analyzing gene expression in human bone marrow -

PT Example 4; SEQ ID NO: 33297; 658pp + Sequence Listing; English.

PS The present invention provides a number of single exon nucleic acid

CC probes which are derived from genomic sequences expressed in the human

CC bone marrow. They can be used to measure gene expression in bone marrow

CC samples, which may enable the improved diagnosis and treatment of cancers

CC such as lymphoma, leukaemia and myeloma. The present sequence is a

CC protein encoded by one of the probes of the invention.

XX Sequence 59 AA;

Query Match 16.6%; Score 26; DB 22; Length 59;

Best Local Similarity 30.8%; Pred. No. 1.8e+03;

Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 17 PXXXXXXCXGXC 29

DB 20 PGSSPPSACAGAC 32

RESULT 12

AAM19796

ID AAM19796 standard; Protein: 59 AA.

AC AAM19796;

DT 12-OCT-2001 (first entry)

DE Peptide #6230 encoded by probe for measuring cervical gene expression.

XX Probe: human; microarray; gene expression; cervical epithelial cell;

KW cervical cancer.

XX Homo sapiens.

PN W0200157278-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US00670.  
 XX  
 PR 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 DR WPI; 2001-488901/53.  
 XX  
 PT Human genome-derived single exon nucleic acid probes useful for  
 PT analyzing gene expression in human cervical epithelial cells -  
 XX  
 PS Claim 27; SEQ ID No 24622; 487pp; English.  
 XX  
 CC The present invention relates to human single exon nucleic acid probes  
 CC (SENP: see A110068-A18459). The present sequence is a peptide encoded  
 CC by one such probe. The SENPs are derived from human Hela cells. The SENPs  
 CC can be used to produce a single exon microarray, which can be used for  
 CC measuring human gene expression in a sample derived from human cervical  
 CC epithelial cells. By measuring gene expression, the probes are therefore  
 CC useful in grading and/or staging of diseases of the cervix, notably  
 CC cervical cancer.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 CC  
 SQ Sequence 59 AA:  
 Query Match 16.6%; Score 26; DB 22; Length 59;  
 Best Local Similarity 30.8%; Pred. No. 1.8e+03;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 QY 17 PXXXXXXXXCXGC 29  
 DB 20 PGSSPPSACAGAC 32  
 RESULT 13  
 AAM33215  
 ID AAM33215 standard; Protein; 59 AA.  
 AC  
 XX  
 XX AAM33215;  
 DT 17-OCT-2001 (first entry)  
 XX  
 DE Peptide #7252 encoded by probe for measuring placental gene expression.  
 XX  
 KW Probe; microarray; human; placenta; antenatal diagnosis;  
 KW genetic disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200157272-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US00663.  
 XX  
 PR 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 DR WPI; 2001-488901/53.  
 XX  
 PT Human genome-derived single exon nucleic acid probes useful for  
 PT analyzing gene expression in human placenta -  
 XX  
 PS Claim 27; SEQ ID No 33484; 654pp; English.  
 XX  
 CC The present invention relates to single exon nucleic acid probes (SENP:  
 CC see A11315-A157546). The present sequence is a peptide encoded by one  
 CC such probe. The probes are useful for producing a microarray for  
 CC predicting, measuring and displaying gene expression in samples derived  
 CC from human placenta. The probes are useful for antenatal diagnosis of  
 CC human genetic disorders.  
 CC  
 SQ Sequence 59 AA:  
 Query Match 16.6%; Score 26; DB 22; Length 59;  
 Best Local Similarity 30.8%; Pred. No. 1.8e+03;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 QY 17 PXXXXXXXXCXGC 29  
 DB 20 PGSSPPSACAGAC 32  
 RESULT 14  
 ABG42830  
 ID ABG42830 standard; Peptide; 59 AA.  
 AC  
 XX  
 XX ABG42830;  
 DT 19-AUG-2002 (first entry)  
 XX  
 DE Human peptide encoded by genome-derived single exon probe SEQ ID 32495.  
 XX  
 KW Human; single exon probe; asthma; lung cancer; COPD; ILD;  
 KW chronic obstructive pulmonary disease; interstitial lung disease;  
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;  
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;  
 KW Hermansky-Rudrak syndrome; sarcoidosis; pulmonary haemosiderosis;  
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karsenger syndrome;  
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;  
 KW primary ciliary dyskinesia; pulmonary hypertension;  
 KW hyaline membrane disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200186003-A2.  
 XX  
 PD 15-NOV-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US00665.  
 XX  
 PR 04-FEB-2000; 2000US-180312P.  
 PR 26-MAY-2000; 2000US-207456P.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-234687P.  
 PR 27-SEP-2000; 2000US-236359P.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX

DR WPI: 2002-114183/15.  
 XX Spatially-addressable set of single exon nucleic acid probes, used to  
 PT measure gene expression in human lung samples -  
 XX  
 PS Claim 27; SEQ ID No 32495; 634bp; English.  
 CC The invention relates to a spatially-addressable set of single exon  
 CC nucleic acid probes for measuring gene expression in a sample derived  
 CC from human lung comprising single exon nucleic acid probes having one of  
 CC 12614 nucleic acid sequences mentioned in the specification, or their  
 CC complements or the 12387 open reading frames derived from the 12614  
 CC probes. Also included are a microarray comprising the novel set of  
 CC probes; the novel set of probes which hybridise at high stringency to a  
 CC nucleic acid expressed in the human lung; measuring gene expression in a  
 CC sample derived from human lung, comprising (a) contacting the array with  
 CC a collection of detectably labeled nucleic acids derived from human lung  
 CC mRNA, and (b) measuring the label detectably bound to each probe of  
 CC the array; identifying exons in a eukaryotic genome, comprising  
 CC (a) algorithmically predicting at least one exon from genomic sequences  
 CC of the eukaryote; and (b) detecting specific hybridisation of detectably  
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,  
 CC having a fragment identical to the predicted exon, the probe is included  
 CC in the above mentioned microarray; assigning exons to a single gene,  
 CC comprising (a) identifying exons from genomic sequence by the method  
 CC above and (b) measuring the expression of each of the exons in several  
 CC tissues and/or cell types using hybridisation to a single exon  
 CC microarrays having a probe with the exon, where a common pattern of  
 CC expression of the exons in the tissues and/or cell types indicates that  
 CC the exons should be assigned to a single gene; a peptide comprising one  
 CC of 12011 sequences, mentioned in the specification, or encoded by the  
 CC probes/open reading frames (ORF). The probes are used for gene  
 CC expression analysis, and for identifying exons in a gene, particularly  
 CC using human lung derived mRNA and for the study of lung diseases  
 CC such as asthma, lung cancer, chronic obstructive pulmonary disease  
 CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary  
 CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,  
 CC Niemann-Pick disease, Hermansky-Rudrak syndrome, sarcoidosis, pulmonary  
 CC haemangioendothelioma, pulmonary histiocytosis, lymphangioleiomyomatosis,  
 CC pulmonary alveolar proteinosis, Karsenger syndrome, fibrocystic  
 CC pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension  
 CC and hyaline membrane disease. The present sequence is a peptide/protein  
 CC encoded by a single exon probe of the invention.  
 CC Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic  
 CC format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 CC  
 XX  
 SQ Sequence 59 AA;  
 Query Match 16.6%; Score 26; DB 23; Length 59;  
 Best Local Similarity 30.8%; Pred. No. 1.8e+03;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 Oy 17 PXXXXXXCXGXC 29  
 | | | |  
 Db 20 PESSPPSCAGAC 32  
 RESULT 15  
 AAM30345  
 ID AAM30345 standard; Peptide: 66 AA.  
 XX  
 AC AAM30345;  
 XX  
 DT 11-FEB-1998 (first entry)  
 XX  
 DE Fragment of bone morphogenic factor 3.  
 XX  
 XX Neururin; human; haematopoietic cell; neuronal cell; stem cell; NT gene;  
 KW neurodegenerative disease; peripheral neuropathy; nervous system tumour;  
 KW amyotrophic lateral sclerosis; Alzheimer's disease; Parkinson's disease;  
 KW Huntingdon's disease; ischaemic stroke; acute brain injury; basopenia;

KW acute spinal cord injury; multiple sclerosis; eosinopenia; lymphopenia;  
 KW monocytopenia; neutropenia; anaemia; thrombocytopenia; neuroblastoma;  
 KW antibody; obesity; therapy; bone morphogenic factor 3; growth factor;  
 KW hybrid protein; BMP3.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W09708196-A1.  
 XX  
 PD 06-MAR-1997.  
 XX  
 PF 27-AUG-1996; 96MO-US14065.  
 XX  
 PR 28-AUG-1995; 95US-0519777.  
 XX  
 PA (UNIT) UNIT WASHINGTON.  
 XX  
 PI Johnson EM, Kotzauer PT, Lampe PA, Milbrandt JD;  
 XX  
 DR WPI: 1997-179176/16.  
 XX  
 PT A novel growth factor Neururin - used to treat neuro-degenerative  
 PT and haematopoietic cell degeneration diseases, e.g. Alzheimer's  
 PT disease and eosinopenia  
 XX  
 PS Claim 93; Fig 17; 206bp; English.  
 XX  
 SQ AAM30331-W30353 represent human growth factor fragments that are used in  
 CC a hybrid polypeptide of the invention. These sequences form a hybrid  
 CC with the human neururin (NT) fragment shown in AAM30378. NT promotes the  
 CC growth and differentiation of haematopoietic and neuronal cells, and  
 CC their stem cells. The NT gene and protein are used to prevent or treat  
 CC neurodegenerative diseases e.g. peripheral neuropathy, amyotrophic  
 CC lateral sclerosis, Alzheimer's disease, Parkinson's disease,  
 CC Huntingdon's disease, ischaemic stroke, acute brain injury, acute spinal  
 CC cord injury, nervous system tumours, multiple sclerosis and infection;  
 CC and haematopoietic cell degenerative diseases, e.g. eosinopenia,  
 CC basopenia, lymphopenia, monocytopenia, neutropenia, anaemia,  
 CC thrombocytopenia and stem cell insufficiencies. The NT protein and gene  
 CC are also useful to treat neuroblastomas. Antibodies against NT and  
 CC oligonucleotides (used as either probes or primers, corresponding to an  
 CC exon of pre-pro-NT gene or flanking a target sequence) can be used for  
 CC detecting NT in a sample or detecting mutations in the NT gene. Antisense  
 CC sequences of the NT gene are used to treat diseases promoted by NT  
 CC expression e.g. obesity.  
 CC  
 XX  
 SQ Sequence 66 AA;  
 Query Match 16.6%; Score 26; DB 18; Length 66;  
 Best Local Similarity 30.8%; Pred. No. 2e+03;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 Oy 17 PXXXXXXCXGXC 29  
 | | | |  
 Db 22 PKSFDAVYCSGAC 34

Search completed: March 27, 2003, 10:59:39  
 Job time : 38 secs



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OM protein - protein search, using sw model

Run on: March 27, 2003, 10:59:00 ; Search time 15 Seconds  
(without alignments)  
190.266 Million cell updates/sec

Title: US-09-828-607-6

Perfect score: 157  
Sequence: 1 XXXXXXXXXXXXXXXPPXX.....XXXXXXXXXXXXCXCX 97

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

1: /cgn2\_6/pdata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/pdata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/pdata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/pdata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/pdata/1/1aa/PCTUS.COMB.pep:\*  
6: /cgn2\_6/pdata/1/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	17.8	178	4	US-09-072-596-297
2	26	16.6	103	1	US-08-335-583C-41
3	26	16.6	103	3	US-08-478-097A-11
4	26	16.6	103	4	US-08-931-858E-164
5	26	16.6	103	4	US-08-981-739-164
6	26	16.6	103	4	US-09-128-026-164
7	26	16.6	104	1	US-08-278-729A-26
8	26	16.6	104	1	US-08-155-343A-26
9	26	16.6	104	1	US-08-406-672-26
10	26	16.6	104	1	US-08-643-763A-26
11	26	16.6	104	1	US-08-462-623-26
12	26	16.6	104	1	US-08-912-088-26
13	26	16.6	104	1	US-08-445-467-26
14	26	16.6	104	1	US-08-451-953A-26
15	26	16.6	104	2	US-08-445-468A-26
16	26	16.6	104	2	US-08-461-397A-26
17	26	16.6	104	2	US-08-278-730A-26
18	26	16.6	104	3	US-08-445-467-26
19	26	16.6	104	3	US-08-480-515A-26
20	26	16.6	104	4	US-08-271-556A-13
21	26	16.6	104	4	US-09-170-936-26
22	26	16.6	104	4	US-08-461-113-26
23	26	16.6	104	5	PCT-US93-07190-26
24	26	16.6	104	5	PCT-US93-07231-26
25	26	16.6	104	5	PCT-US93-08742-26
26	26	16.6	104	5	PCT-US93-08808-26
27	26	16.6	104	5	PCT-US93-08885-26

28	26	16.6	109	1	US-07-841-646-21	Sequence 21, Appl
29	26	16.6	109	1	US-07-901-703-17	Sequence 17, Appl
30	26	16.6	109	1	US-08-147-023-17	Sequence 21, Appl
31	26	16.6	109	1	US-08-447-570-21	Sequence 21, Appl
32	26	16.6	109	2	US-08-449-700-21	Sequence 21, Appl
33	26	16.6	109	2	US-08-449-699A-21	Sequence 21, Appl
34	26	16.6	109	5	PCT-US93-05446-17	Sequence 21, Appl
35	26	16.6	115	4	US-08-624-635-25	Sequence 25, Appl
36	26	16.6	115	4	US-08-624-635-26	Sequence 26, Appl
37	26	16.6	119	1	US-08-481-377-18	Sequence 18, Appl
38	26	16.6	119	2	US-08-491-835-16	Sequence 16, Appl
39	26	16.6	119	3	US-09-153-733A-18	Sequence 18, Appl
40	26	16.6	119	3	US-08-946-092A-16	Sequence 16, Appl
41	26	16.6	119	4	US-09-172-062-16	Sequence 16, Appl
42	26	16.6	119	4	US-09-301-520D-16	Sequence 16, Appl
43	26	16.6	119	4	US-09-389-705-18	Sequence 18, Appl
44	26	16.6	119	5	PCT-US94-00666-18	Sequence 18, Appl
45	26	16.6	119	5	PCT-US94-00685-16	Sequence 16, Appl

#### ALIGNMENTS

RESULT 1  
US-09-072-596-297  
; Sequence 297, Application US/09072596  
; Patent No. 6458366  
; GENERAL INFORMATION:  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Skelky, Yastir A.W.  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Campos-Neto, Antonia  
; APPLICANT: Houghton, Raymond  
; APPLICANT: Vedicik, Thomas S.  
; APPLICANT: Twardzik, Daniel R.  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Hendrickson, Ronald C.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF  
; NUMBER OF SEQUENCES: 350  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/072,596  
; FILING DATE: 05-MAY-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 210121.417C9  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 297:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 178 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-072-596-297  
; Query Match 17.8%; Score 28; DB 4; Length 178;  
; Best Local Similarity 30.8%; Pred. No. 3,4e+02;

Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 17 PXXXXXXCXGC 29  
DB 103 PAAAAQJCRGSC 115

RESULT 2  
US-08-335-583C-41  
; Sequence 41, Application US/08335583C  
; Patent No. 5693779  
; GENERAL INFORMATION:  
; APPLICANT: MOOS JR., MALCOLM  
; APPLICANT: Wang, Shouwan  
; APPLICANT: Krinks, Marie  
; TITLE OF INVENTION: PRODUCTION AND USE OF  
; TITLE OF INVENTION: ANTI-DORSALIZING MORPHOGENETIC PROTEIN  
; NUMBER OF SEQUENCES: 56  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobb, Martens, Olson and Bear  
; STREET: 620 Newport Center Drive 16th floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ Version 1.5  
; CURRENT APPLICATION DATA: US/08/335,583C  
; APPLICATION NUMBER: US/08/335,583C  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Altman, Daniel E  
; REGISTRATION NUMBER: 34,115  
; REFERENCE/DOCKET NUMBER: NIH104,001A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 714-760-0404  
; TELEFAX: 714-760-9502  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 41:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 103 amino acids  
; TYPE: amino acids  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: C-terminal  
; ORIGINAL SOURCE:  
US-08-335-583C-41  
Query Match 16.6%; Score 26; DB 1; Length 103;  
Best Local Similarity 30.8%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 17 PXXXXXXCXGC 29  
DB 22 PKSFDAYCSGAC 34  
RESULT 3  
US-08-478-097A-11  
; Sequence 11, Application US/08478097A  
; Patent No. 6040431  
; GENERAL INFORMATION:  
; APPLICANT: KECK, PETER

APPLICANT: SMART, JOHN  
; TITLE OF INVENTION: SINGLE-CHAIN ANALOGS OF TGF-B  
; TITLE OF INVENTION: SUPERFAMILY (MORPHONS)  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &  
; ADDRESSEE: THIBEAULT, LLP  
; STREET: 125 HIGH STREET  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/478,097A  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PITCHER, ESO, EDMUND R  
; REGISTRATION NUMBER: 27,829  
; REFERENCE/DOCKET NUMBER: CRP-080  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-248-7000  
; TELEFAX: 617-248-7100  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 103 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..103  
; OTHER INFORMATION: /note="BMP3 SEQUENCE"  
US-08-478-097A-11  
Query Match 16.6%; Score 26; DB 3; Length 103;  
Best Local Similarity 30.8%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 17 PXXXXXXCXGC 29  
DB 22 PKSFDAYCSGAC 34  
RESULT 4  
US-08-931-858E-164  
; Sequence 164, Application US/08931858E  
; Patent No. 6222022  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON, EUGENE M  
; APPLICANT: MILBRANDT, JEFFREY D  
; APPLICANT: KOTZBAUER, PAUL T  
; APPLICANT: LAMPE, PATRICIA A  
; APPLICANT: KLEIN, ROBERT  
; APPLICANT: DESAUVAGE, FRED  
; TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR  
; NUMBER OF SEQUENCES: 239  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOWELL & HAERKAMP, L.C.  
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MO  
; COUNTRY: USA  
; ZIP: 63105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/931,858E  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 971486  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 314-727-5188  
TELEFAX: 314-727-6092  
INFORMATION FOR SEQ ID NO: 164:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 103 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-931-858E-164

Query Match  
Best Local Similarity 16.6%; Score 26; DB 4; Length 103;  
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29  
DB 22 PKSPDAYYCSGAC 34

RESULT 5  
US-08-981-739-164  
Sequence 164, Application US/08981739  
Patent No. 6232449  
GENERAL INFORMATION:  
APPLICANT: JOHNSON JR., EUGENE M.  
MILBRANDT, JEFFREY D.  
KOTZBAUER, PAUL T.  
LAMPE, PATRICIA A.  
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS  
NUMBER OF SEQUENCES: 176  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
CITY: ST. LOUIS  
STATE: MISSOURI  
COUNTRY: US  
ZIP: 63105-1817  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/981,739  
FILING DATE: 31-Aug-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCW/US97/03461  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 976163  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 727-5188  
TELEFAX: (314) 727-6092  
INFORMATION FOR SEQ ID NO: 164:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 103 amino acids  
TYPE: amino acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 164:  
US-08-981-739-164

Query Match  
Best Local Similarity 16.6%; Score 26; DB 4; Length 103;  
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29  
DB 22 PKSPDAYYCSGAC 34

RESULT 6  
US-09-128-026-164  
Sequence 164, Application US/09128026  
Patent No. 640335  
GENERAL INFORMATION:  
APPLICANT: JOHNSON JR., EUGENE M.  
MILBRANDT, JEFFREY D.  
KOTZBAUER, PAUL T.  
APPLICANT: LAMPE, PATRICIA A.  
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS  
NUMBER OF SEQUENCES: 176  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
CITY: ST. LOUIS  
STATE: MISSOURI  
COUNTRY: US  
ZIP: 63105-1817  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/128,026  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 976163  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 727-5188  
TELEFAX: (314) 727-6092  
INFORMATION FOR SEQ ID NO: 164:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 103 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-128-026-164

Query Match  
Best Local Similarity 16.6%; Score 26; DB 4; Length 103;  
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29  
DB 22 PKSPDAYYCSGAC 34

RESULT 7  
US-08-278-729A-26  
Sequence 26, Application US/08278729A  
Patent No. 5650276  
GENERAL INFORMATION:  
APPLICANT: SMART, JOHN  
APPLICANT: OPPERMANN, HERMAN

APPLICANT: OZKAYNAK, ENGİN  
APPLICANT: KUBERASAMPATH, THANGAVEL  
APPLICANT: RUEGER, DAVID C.  
APPLICANT: PANG, ROY H.L.  
APPLICANT: COHEN, CHARLES M.  
TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES  
STREET: 45 SOUTH STREET  
CITY: HOPKINTON  
STATE: MA  
COUNTRY: USA  
ZIP: 01748  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/278,729A  
FILING DATE: 20-JUL-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: PITCHER Esq., EDMOND R.  
REGISTRATION NUMBER: 27,829  
REFERENCE/DOCKET NUMBER: CRP-058CPEW  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (508) 435-9001  
TELEFAX: (508) 435-6951  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 104 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..104  
OTHER INFORMATION: /label= BMP3  
US-08-278-729A-26

Query Match 16.6%; Score 26; DB 1; Length 104;  
Best Local Similarity 30.8%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29  
DB 22 PKSFDAYCAGC 34

RESULT 8  
US-08-155-343A-26  
Sequence 26, Application US/08155343A  
Patent No. 5656593  
GENERAL INFORMATION:  
APPLICANT: KUBERASAMPATH, THANGAVEL  
APPLICANT: RUEGER, DAVID C.  
APPLICANT: OPPERMAN, HERMAN  
APPLICANT: COHEN, CHARLES M.  
APPLICANT: PANG, ROY H.L.  
TITLE OF INVENTION: MORPHOGENIC-INDUCED PERIODONTAL TISSUE  
REGENERATION.  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES  
STREET: 45 SOUTH STREET  
CITY: HOPKINTON  
STATE: MA  
COUNTRY: USA  
ZIP: 01748  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/155,343A  
FILING DATE: 15-NOV-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: FENTON Esq., GILLIAN M.  
REGISTRATION NUMBER: 36,508  
REFERENCE/DOCKET NUMBER: CRP-067FW  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7560  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 104 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..104  
OTHER INFORMATION: /label= BMP3  
US-08-155-343A-26

Query Match 16.6%; Score 26; DB 1; Length 104;  
Best Local Similarity 30.8%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29  
DB 22 PKSFDAYCAGC 34

RESULT 9  
US-08-406-672-26  
Sequence 26, Application US/08406672  
Patent No. 56744844  
GENERAL INFORMATION:  
APPLICANT: KUBERASAMPATH, THANGAVEL  
APPLICANT: COHEN, CHARLES M.  
APPLICANT: OPPERMAN, HERMAN  
APPLICANT: OZKAYNAK, ENGİN  
APPLICANT: RUEGER, DAVID C.  
APPLICANT: PANG, ROY H.L.  
TITLE OF INVENTION: TREATMENT TO PREVENT LOSS OF AND/OR  
INCREASE BONE MASS IN METABOLIC BONE DISEASES  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES  
STREET: 45 SOUTH STREET  
CITY: HOPKINTON  
STATE: MA  
COUNTRY: USA  
ZIP: 01748  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/406,672  
FILING DATE: 20-MAR-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 752,857  
FILING DATE: 30-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 667,274  
FILING DATE: 11-MAR-1991

ATTORNEY/AGENT INFORMATION:  
NAME: FENTON Esq., GILLIAN M.  
REGISTRATION NUMBER: 36,508  
REFERENCE/DOCKET NUMBER: CRP-060CN  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7100  
TELEFAX: (617) 248-7560  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 104 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..104  
OTHER INFORMATION: /label= BMP3  
US-08-406-672-26

Query Match 16.6%; Score 26; DB 1; Length 104;  
Best Local Similarity 30.8%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 17 PXXXXXXCXGC 29  
DB 22 PKSFDAVYCSGAC 34

RESULT 10  
US-08-643-563A-26

Sequence 26, Application US/08643563A  
Patent No. 5707810

GENERAL INFORMATION:

APPLICANT: SMART, JOHN

APPLICANT: OPPERMAN, HERMAN

APPLICANT: OZKAYNAK, ENGIN

APPLICANT: KUBERASAMPATH, THANGAVEL

APPLICANT: RUEGER, DAVID C.

APPLICANT: PANG, ROY H.L.

APPLICANT: COHEN, CHARLES M.

TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES

STREET: 45 SOUTH STREET

CITY: HOPKINTON

STATE: MA

COUNTRY: USA

ZIP: 01748

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/643,563A

FILING DATE: 06-MAY-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: TWOMEY Esq., MICHAEL J.

REGISTRATION NUMBER: 38,349

REFERENCE/DOCKET NUMBER: CRP-058CN2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (508) 435-9901

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

LENGTH: 104 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..104  
OTHER INFORMATION:  
US-08-643-563A-26 /label= BMP3

Query Match 16.6%; Score 26; DB 1; Length 104;  
Best Local Similarity 30.8%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 17 PXXXXXXCXGC 29  
DB 22 PKSFDAVYCSGAC 34

RESULT 11

US-08-643-763A-26

Sequence 26, Application US/08643763A  
Patent No. 5733878

GENERAL INFORMATION:

APPLICANT: KUBERASAMPATH, THANGAVEL

APPLICANT: RUEGER, DAVID C.

APPLICANT: OPPERMAN, HERMAN

APPLICANT: COHEN, CHARLES M.

APPLICANT: PANG, ROY H.L.

TITLE OF INVENTION: MORPHOGENIC-INDUCED PERIODONTAL TISSUE

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES

STREET: 45 SOUTH STREET

CITY: HOPKINTON

STATE: MA

COUNTRY: USA

ZIP: 01748

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/643,763A

FILING DATE: 06-MAY-1996

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: FENTON Esq., GILLIAN M.

REGISTRATION NUMBER: 36,508

REFERENCE/DOCKET NUMBER: CRP-067CN

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 248-7100

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

LENGTH: 104 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: Protein

LOCATION: 1..104

OTHER INFORMATION: /label= BMP3  
US-08-643-763A-26

Query Match 16.6%; Score 26; DB 1; Length 104;  
Best Local Similarity 30.8%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 17 PXXXXXXCXGC 29  
DB 22 PKSFDAVYCSGAC 34

RESULT 12  
US-08-462-623-26  
Sequence 26, Application US/08462623  
Patent No. 5739107  
GENERAL INFORMATION:  
APPLICANT: COHEN, CHARLES M.  
APPLICANT: CHARETTE, MARC F.  
APPLICANT: KUBERASAMPATH, THANGAVEL  
APPLICANT: RUEGER, DAVID C.  
APPLICANT: OPPERMAN, HERMANN  
APPLICANT: PANG, ROY H.L.  
APPLICANT: OKAYNAK, ENGIN  
APPLICANT: SMART, JOHN E.  
TITLE OF INVENTION: MORPHOGEN TREATMENT OF GASTROINTESTINAL  
TITLE OF INVENTION: ULCERS.  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES  
STREET: 45 SOUTH STREET  
CITY: HOPKINTON  
STATE: MA  
COUNTRY: USA  
ZIP: 01748  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/462,623  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/445,882  
FILING DATE: 22-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: FENTON ESQ., GILLIAN M.  
REGISTRATION NUMBER: 36,508  
REFERENCE/DOCKET NUMBER: CRP-074CN  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (508) 435-9001  
TELEFAX: (508) 435-6951  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 104 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..104  
OTHER INFORMATION: /label= BMP3  
US-08-462-623-26  
Query Match 16.6%; Score 26; DB 1; Length 104;  
Best Local Similarity 30.8%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 17 PXXXXXXXXXXC 29  
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Db 22 PKSFDAYCAGC 34

RESULT 13  
US-08-451-953A-26  
Sequence 26, Application US/08451953A  
Patent No. 5741641  
GENERAL INFORMATION:  
APPLICANT: SMART, JOHN  
APPLICANT: OPPERMAN, HERMANN  
APPLICANT: OKAYNAK, ENGIN  
APPLICANT: KUBERASAMPATH, THANGAVEL

APPLICANT: RUEGER, DAVID C.  
APPLICANT: PANG, ROY H.L.  
APPLICANT: COHEN, CHARLES M.  
TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES  
STREET: 45 SOUTH STREET  
CITY: HOPKINTON  
STATE: MA  
COUNTRY: USA  
ZIP: 01748  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/451,953A  
FILING DATE: 26-MAY-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: PITCHER ESQ., EDWARD R.  
REGISTRATION NUMBER: 27,829  
REFERENCE/DOCKET NUMBER: CRP-058CN  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (508) 435-9001  
TELEFAX: (508) 435-6951  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 104 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..104  
OTHER INFORMATION: /label= BMP3  
US-08-451-953A-26  
Query Match 16.6%; Score 26; DB 1; Length 104;  
Best Local Similarity 30.8%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 17 PXXXXXXXXXXC 29  
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Db 22 PKSFDAYCAGC 34

RESULT 14  
US-08-445-468A-26  
Sequence 26, Application US/08445468A  
Patent No. 5849686  
GENERAL INFORMATION:  
APPLICANT: KUBERASAMPATH, THANGAVEL  
APPLICANT: RUEGER, DAVID C.  
APPLICANT: OPPERMAN, HERMANN  
APPLICANT: PANG, ROY H.L.  
APPLICANT: COHEN, CHARLES M.  
TITLE OF INVENTION: MORPHOGEN-INDUCED LIVER REGENERATION  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES  
STREET: 45 SOUTH STREET  
CITY: HOPKINTON  
STATE: MA  
COUNTRY: USA  
ZIP: 01748  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/445,468A  
FILING DATE: 22-MAY-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: FENTON ESQ., GILLIAN M.  
REGISTRATION NUMBER: 36,508  
REFERENCE/DOCKET NUMBER: CRP-072FW2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7560  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 104 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..104  
OTHER INFORMATION: /label= BMP3  
US-08-445-468A-26

Query Match 16.6% Score 26; DB 2; Length 104;  
Best Local Similarity 30.8%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29  
DB 22 PKSPDAYCSGAC 34

RESULT 15  
US-08-461-397A-26  
Sequence 26; Application US/08461397A  
Patent No. 5972884  
GENERAL INFORMATION:  
APPLICANT: COHEN, CHARLES M.  
APPLICANT: CHARETTE, MARC F.  
APPLICANT: KUBERASAMPATH, THANGAVEL  
APPLICANT: RUGGER, DAVID C.  
APPLICANT: OPPERMAN, HERMANN  
APPLICANT: PANG, ROY H.L.  
APPLICANT: OZKAYNAK, ENGIN  
APPLICANT: SMART, JOHN E.  
TITLE OF INVENTION: MORPHOGEN TREATMENT FOR LIMITING  
TITLE OF INVENTION: PROLIFERATION OF EPITHELIAL CELLS.  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES  
STREET: 45 SOUTH STREET  
CITY: HOPKINTON  
STATE: MA  
COUNTRY: USA  
ZIP: 01748  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,397A  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: PITCHER ESQ., EDMUND R.  
REGISTRATION NUMBER: 27,829  
REFERENCE/DOCKET NUMBER: CRP-074FW2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/248-7000  
TELEFAX: 617/248-7100

INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 104 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..104  
OTHER INFORMATION: /label= BMP3  
US-08-461-397A-26

Query Match 16.6% Score 26; DB 2; Length 104;  
Best Local Similarity 30.8%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29  
DB 22 PKSPDAYCSGAC 34

Search completed: March 27, 2003, 11:02:54  
Job time : 16 secs





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## OM protein - protein search, using sw model

Run on: March 27, 2003, 10:59:45 ; Search time 14 Seconds

(Without alignments)  
406,871 Million cell updates/sec

Title: US-09-828-607-6

Perfect score: 157  
Sequence: 1 XX 97Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 237916 seqs, 58723674 residues

Total number of hits satisfying chosen parameters: 237916

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

Published Applications AA:\*  
1: /cgn2\_6/ptodata/2/pubppa/US08\_NEW\_PUB.pep.\*  
2: /cgn2\_6/ptodata/2/pubppa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubppa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubppa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubppa/US07\_NEW\_PUB.pep.\*  
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14: /cgn2\_6/ptodata/2/pubppa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	27	17.2	2609	9	US-10-184-644-407
3	27	17.2	2870	9	US-10-184-644-473
4	26	16.6	59	10	US-09-864-761-39622
5	26	16.6	84	10	US-09-995-515-8
6	26	16.6	115	10	US-09-813-459-25
7	26	16.6	115	10	US-09-813-459-26
8	26	16.6	119	12	US-10-115-406-16
9	26	16.6	120	9	US-09-859-211-42
10	26	16.6	120	9	US-09-880-708-20
11	26	16.6	120	10	US-09-813-459-6
12	26	16.6	120	10	US-09-813-459-16
13	26	16.6	131	10	US-09-995-515-12
14	26	16.6	140	10	US-09-995-515-2
15	26	16.6	182	9	US-09-974-879-139
16	26	16.6	195	10	US-09-995-515-4
17	26	16.6	212	9	US-09-949-192-29
18	26	16.6	473	9	US-09-813-398-25
19	26	16.6	476	10	US-09-813-459-5

20	26	16.6	479	9	US-09-813-398-26	Sequence 26, App1
21	26	16.6	2121	9	US-10-184-644-355	Sequence 355, App
22	26	16.6	4440	9	US-10-174-590-525	Sequence 525, App
23	26	16.6	4440	9	US-10-176-758-525	Sequence 525, App
24	26	16.6	4440	9	US-10-175-737-525	Sequence 525, App
25	26	16.6	4440	9	US-10-173-706-525	Sequence 525, App
26	26	16.6	4440	9	US-10-175-738-525	Sequence 525, App
27	26	16.6	4440	9	US-10-175-752-525	Sequence 525, App
28	26	16.6	4440	9	US-10-176-487-525	Sequence 525, App
29	26	16.6	4440	9	US-10-176-757-525	Sequence 525, App
30	26	16.6	4440	9	US-10-176-913-525	Sequence 525, App
31	26	16.6	4440	9	US-10-180-552-525	Sequence 525, App
32	26	16.6	4440	9	US-10-180-557-525	Sequence 525, App
33	26	16.6	4440	9	US-10-173-700-525	Sequence 525, App
34	26	16.6	4440	9	US-10-174-572-525	Sequence 525, App
35	26	16.6	4440	9	US-10-174-572-525	Sequence 525, App
36	26	16.6	4440	9	US-10-174-582-525	Sequence 525, App
37	26	16.6	4440	9	US-10-174-588-525	Sequence 525, App
38	26	16.6	4440	9	US-10-175-739-525	Sequence 525, App
39	26	16.6	4440	9	US-10-175-740-525	Sequence 525, App
40	26	16.6	4440	9	US-10-175-743-525	Sequence 525, App
41	26	16.6	4440	9	US-10-176-488-525	Sequence 525, App
42	26	16.6	4440	9	US-10-176-492-525	Sequence 525, App
43	26	16.6	4440	9	US-10-176-747-525	Sequence 525, App
44	26	16.6	4440	9	US-10-176-750-525	Sequence 525, App
45	26	16.6	4440	9	US-10-176-985-525	Sequence 525, App

## ALIGNMENTS

RESULT 1  
US-09-801-368-358  
Sequence 358, Application US/09801368  
Patent No. US20020128250A1  
GENERAL INFORMATION:  
APPLICANT: Busby, Robert  
APPLICANT: Call, Brian  
APPLICANT: Hecht, Peter  
APPLICANT: Holtzman, Doug  
APPLICANT: Madden, Kevin  
APPLICANT: Maxon, Mary  
APPLICANT: Milne, Todd  
APPLICANT: Royer, John  
APPLICANT: Salama, Sofie  
APPLICANT: Sherman, Amir  
APPLICANT: Silva, Jeff  
APPLICANT: Summers, Eric  
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi  
FILE REFERENCE: 109272.147  
CURRENT APPLICATION NUMBER: US/09/801,368  
PRIORITY FILING DATE: 2001-03-07  
PRIORITY FILING DATE: 2000-01-19  
PRIORITY FILING DATE: 1999-10-20  
NUMBER OF SEQ ID NOS: 440  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 358  
LENGTH: 549  
TYPE: PRT  
ORGANISM: Aspergillus nidulans  
US-09-801-368-358

Query Match 17.2% Score 27; DB 10; Length 549;

Best Local Similarity 30.8%; Pred. No. 1.6e+03; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 9;

QY 17 PXXXXXXXXXXGXC 29  
DB 168 PAVTSGECTGSC 180

## RESULT 2

US-10-184-644-407  
Sequence 407, Application US/10184644  
Publication No. US20030044930A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Chen, Jian  
APPLICANT: Desnoyers, Luc  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Pan, James  
APPLICANT: Smith, Victoria  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3430R1C227  
CURRENT APPLICATION NUMBER: US/10/184,644  
PRIORITY FILING DATE: 2002-06-28  
Prior Application removed - See file wrapper or Palm  
NUMBER OF SEQ ID NOS: 612  
SEQ ID NO 407  
LENGTH: 2609  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-184-644-407

Query Match 17.2%; Score 27; DB 9; Length 2609;  
Best Local Similarity 10.5%; Pred. No. 4.3e+03;  
Matches 4; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 25 CXGXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 62

DB 2393 CCGCTGTCATTTTGAGATTTTAAAAAATATGTC 2430

## RESULT 3

US-10-184-644-473  
Sequence 473, Application US/10184644  
Publication No. US20030044930A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Chen, Jian  
APPLICANT: Desnoyers, Luc  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Pan, James  
APPLICANT: Smith, Victoria  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3430R1C227  
CURRENT APPLICATION NUMBER: US/10/184,644  
PRIORITY FILING DATE: 2002-06-28  
Prior Application removed - See file wrapper or Palm  
NUMBER OF SEQ ID NOS: 612  
SEQ ID NO 473  
LENGTH: 2870  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-184-644-473

Query Match 17.2%; Score 27; DB 9; Length 2870;  
Best Local Similarity 10.5%; Pred. No. 4.6e+03;  
Matches 4; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 25 CXGXCXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 62

DB 2823 CCGCTTTTACTTTTAACGATATTAATGATATC 2860

## RESULT 4

US-09-864-761-39622  
Sequence 39622, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
FILE REFERENCE: Aecm13-X-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
PRIORITY FILING DATE: 2001-05-23  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263,6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 39622  
LENGTH: 59  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AC005809.1  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.1  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.5  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 66  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.3  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 8.4  
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.1  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 6.4  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 5.1  
OTHER INFORMATION: SWISSPROT HIT: 076942, EVALUATION 1.60e+00

US-09-864-761-39622

Query Match 16.6%; Score 26; DB 10; Length 59;  
Best Local Similarity 30.8%; Pred. No. 5e+02;  
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 17 PXXXXXXCXGC 29  
DB 20 PGSSPPSACAGAC 32

## RESULT 5

US-09-995-515-8  
; Sequence 8, Application US/09995515  
; Patent No. US20020151695A1  
; GENERAL INFORMATION:  
; APPLICANT: Jing, Shugian  
; TITLE OF INVENTION: Transforming Growth Factor-Beta-Related Molecules and  
; FILE REFERENCE: 00-659-7  
; CURRENT APPLICATION NUMBER: US/09/995,515  
; PRIOR FILING DATE: 2001-11-28  
; PRIOR APPLICATION NUMBER: 60/253,476  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 84  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-995-515-8

Query Match 16.6%; Score 26; DB 10; Length 84;  
Best Local Similarity 30.8%; Pred. No. 6.4e+02;  
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 17 PXXXXXXCXGC 29  
DB 56 PRTLSFYCQCTC 68

## RESULT 6

US-09-813-459-25  
; Sequence 25, Application US/09813459  
; Patent No. US20020107369A1  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Se-jin  
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-10  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Spensley Horn Judas & Lubitz  
; STREET: 1880 Century Park East, Suite 500  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90067  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/813,459  
; FILING DATE: 20-Mar-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/624,635  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wetherell, Jr., Ph.D., John R.,  
; REGISTRATION NUMBER: 31,678  
; REFERENCE/DOCKET NUMBER: PD-3054  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 455-5100

TELEFAX: (619) 455-5110  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 115 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; IMMEDIATE SOURCE:  
; CLONE: Human GDF-10  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..115  
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:

US-09-813-459-25

Query Match 16.6%; Score 26; DB 10; Length 115;  
Best Local Similarity 30.8%; Pred. No. 7.9e+02;  
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 17 PXXXXXXCXGC 29  
DB 34 PKSFDAIYCAGAC 46

## RESULT 7

US-09-813-459-26  
; Sequence 26, Application US/09813459  
; Patent No. US20020107369A1  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Se-jin  
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-10  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Spensley Horn Judas & Lubitz  
; STREET: 1880 Century Park East, Suite 500  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90067  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/813,459  
; FILING DATE: 20-Mar-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/624,635  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wetherell, Jr., Ph.D., John R.,  
; REGISTRATION NUMBER: 31,678  
; REFERENCE/DOCKET NUMBER: PD-3054  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 455-5100  
; TELEFAX: (619) 455-5110  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 115 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; IMMEDIATE SOURCE:  
; CLONE: Murine GDF-10  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..115  
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:

US-09-813-459-26

Query Match  
Best Local Similarity 16.6%; Score 26; DB 10; Length 115;  
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29  
DB 34 PKSFDAVYCSGAC 46

RESULT 8

US-10-115-406-16  
Sequence 16, Application US/10115406  
Patent No. US20020127612A1  
GENERAL INFORMATION:  
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
APPLICANT: Lee, Se-jin  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9  
FILE REFERENCE: JH01190-3  
CURRENT APPLICATION NUMBER: US/10/115,406  
CURRENT FILING DATE: 2002-04-02  
PRIOR APPLICATION NUMBER: 09/301,520  
PRIOR FILING DATE: 1999-04-28  
PRIOR APPLICATION NUMBER: US 09/172,062  
PRIOR FILING DATE: 1998-10-13  
PRIOR APPLICATION NUMBER: US 08/491,835  
PRIOR FILING DATE: 1995-10-23  
PRIOR APPLICATION NUMBER: PCT/US94/00685  
PRIOR FILING DATE: 1994-01-12  
PRIOR APPLICATION NUMBER: US 08/003,303  
PRIOR FILING DATE: 1993-01-12  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 16  
LENGTH: 119  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-115-406-16

Query Match  
Best Local Similarity 16.6%; Score 26; DB 12; Length 119;  
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29  
DB 38 PKSFDAVYCSGAC 50

RESULT 9

US-09-859-211-42  
Sequence 42, Application US/09859211  
Patent No. US20020157125A1  
GENERAL INFORMATION:  
APPLICANT: Lee, Se-jin  
APPLICANT: McPherron, Alexandra C.  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8  
FILE REFERENCE: 07265/14401  
CURRENT APPLICATION NUMBER: US/09/859,211  
CURRENT FILING DATE: 2001-05-15  
PRIOR APPLICATION NUMBER: 09/019,070  
PRIOR FILING DATE: 1998-02-05  
PRIOR APPLICATION NUMBER: 08/862,445  
PRIOR FILING DATE: 1997-05-23  
PRIOR APPLICATION NUMBER: 08/847,910  
PRIOR FILING DATE: 1997-04-28  
PRIOR APPLICATION NUMBER: 08/795,071  
PRIOR FILING DATE: 1997-02-05  
PRIOR APPLICATION NUMBER: 08/525,596  
PRIOR FILING DATE: 1995-10-26  
PRIOR APPLICATION NUMBER: PCT/US94/03019  
PRIOR FILING DATE: 1994-03-18  
PRIOR APPLICATION NUMBER: 08/033,923

PRIOR FILING DATE: 1993-03-19  
NUMBER OF SEQ ID NOS: 51  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 42  
LENGTH: 120  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-859-211-42

Query Match  
Best Local Similarity 16.6%; Score 26; DB 9; Length 120;  
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29  
DB 39 PKSFDAVYCSGAC 51

RESULT 10

US-09-880-708-20  
Sequence 20, Application US/09880708  
Patent No. US20020165361A1  
GENERAL INFORMATION:  
APPLICANT: Lee, Se-jin  
Huyhn, Thanh  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Gray Cary Ware & Freidenrich LLP  
STREET: 4365 Executive Drive, Suite 1600  
CITY: San Diego  
STATE: CA  
COUNTRY: USA  
ZIP: 92121-2189  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/880,708  
FILING DATE: 12-Jun-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/145,060  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/003,144  
FILING DATE: 12-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Lisa A. Haile, Ph.D.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07265/057002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 858/677-1456  
TELEFAX: 619/677-1465  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: BMP-3  
SEQUENCE DESCRIPTION: SEQ ID NO: 20:  
US-09-880-708-20

Query Match  
Best Local Similarity 16.6%; Score 26; DB 9; Length 120;  
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29  
DB 39 PKSFDAVYCSGAC 51

RESULT 11  
US-09-813-459-6  
Sequence 6, Application US/09813459  
Patent No. US20020107369A1  
GENERAL INFORMATION:  
APPLICANT: Lee, Se-Jin  
Cunningham, No. US20020107369A1  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-10  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Spensley Horn Jubas & Lubitz  
STREET: 1880 Century Park East, Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/813,459  
FILING DATE: 20-Mar-2001  
CLASSIFICATION: <Unknown>  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/624,635  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Wetherell, Jr., Ph.D., John R.,  
REGISTRATION NUMBER: 31,678  
REFERENCE/DOCKET NUMBER: PD-3054  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: GDF-10  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..120  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-813-459-6  
Query Match 16.6%; Score 26; DB 10; Length 120;  
Best Local Similarity 30.8%; Pred. No. 8.1e+02;  
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 17 PXXXXXXCXGC 29  
DB 39 PKSFDAYCAGAC 51  
RESULT 12  
US-09-813-459-16  
Sequence 16, Application US/09813459  
Patent No. US20020107369A1  
GENERAL INFORMATION:  
APPLICANT: Lee, Se-Jin  
Cunningham, No. US20020107369A1  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-10  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Spensley Horn Jubas & Lubitz  
STREET: 1880 Century Park East, Suite 500  
CITY: Los Angeles

STATE: California  
COUNTRY: USA  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/813,459  
FILING DATE: 20-Mar-2001  
CLASSIFICATION: <Unknown>  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/624,635  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Wetherell, Jr., Ph.D., John R.,  
REGISTRATION NUMBER: 31,678  
REFERENCE/DOCKET NUMBER: PD-3054  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: BMP-3  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..120  
SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
US-09-813-459-16  
Query Match 16.6%; Score 26; DB 10; Length 120;  
Best Local Similarity 30.8%; Pred. No. 8.1e+02;  
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 17 PXXXXXXCXGC 29  
DB 39 PKSFDAYCAGAC 51  
RESULT 13  
US-09-995-515-12  
Sequence 12, Application US/0995515  
Patent No. US20020151695A1  
GENERAL INFORMATION:  
APPLICANT: Jing, Shuguan  
TITLE OF INVENTION: Transforming Growth Factor-Beta-Related Molecules and  
FIDE REFERENCE: 00-659-A  
CURRENT FILING DATE: 2001-11-28  
PRIOR APPLICATION NUMBER: 60/253,476  
PRIOR FILING DATE: 2000-11-28  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 12  
LENGTH: 131  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-995-515-12  
Query Match 16.6%; Score 26; DB 10; Length 131;  
Best Local Similarity 30.8%; Pred. No. 8.6e+02;  
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 17 PXXXXXXCXGC 29

Db 103 PKTISFYCGTC 115

RESULT 14

US-09-995-515-2

; Sequence 2, Application US/09995515

; Patent No. US20020151695A1

; GENERAL INFORMATION:

; APPLICANT: Jiny, Shugian

; TITLE OF INVENTION: Transforming Growth Factor-Beta-Related Molecules and

; FILE REFERENCE: 00-659-A

; CURRENT APPLICATION NUMBER: US/09/995,515

; CURRENT FILING DATE: 2001-11-28

; PRIOR APPLICATION NUMBER: 60/253,476

; PRIOR FILING DATE: 2000-11-28

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: Patentln Ver. 2.0

; SEQ ID NO 2

; LENGTH: 140

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-995-515-2

Query Match 16.6%; Score 26; DB 10; Length 140;

Best Local Similarity 30.8%; Pred. No. 9e+02;

Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGC 29

Db 64 PKTISFYCGTC 76

RESULT 15

US-09-974-879-139

; Sequence 139, Application US/09974879

; Publication No. US20030028003A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 125 Human Secreted Proteins

; FILE REFERENCE: P2020P2

; CURRENT APPLICATION NUMBER: US/09/974,879

; CURRENT FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: US 60/239,893

; PRIOR FILING DATE: 2000-10-13

; PRIOR APPLICATION NUMBER: US 09/818,683

; PRIOR FILING DATE: 2001-03-28

; PRIOR APPLICATION NUMBER: US 09/305,736

; PRIOR FILING DATE: 1999-05-05

; PRIOR APPLICATION NUMBER: PCT/US98/23435

; PRIOR FILING DATE: 1998-11-04

; PRIOR APPLICATION NUMBER: US 60/064,911

; PRIOR FILING DATE: 1997-11-07

; PRIOR APPLICATION NUMBER: US 60/064,912

; PRIOR FILING DATE: 1997-11-07

; PRIOR APPLICATION NUMBER: US 60/064,983

; PRIOR FILING DATE: 1997-11-07

; PRIOR APPLICATION NUMBER: US 60/064,900

; PRIOR FILING DATE: 1997-11-07

; PRIOR APPLICATION NUMBER: US 60/064,988

; PRIOR FILING DATE: 1997-11-07

; PRIOR APPLICATION NUMBER: US 60/064,987

; PRIOR FILING DATE: 1997-11-07

; PRIOR APPLICATION NUMBER: US 60/064,908

; PRIOR FILING DATE: 1997-11-07

; PRIOR APPLICATION NUMBER: US 60/064,984

; PRIOR FILING DATE: 1997-11-07

; PRIOR APPLICATION NUMBER: US 60/064,985

; PRIOR FILING DATE: 1997-11-07

; PRIOR APPLICATION NUMBER: US 60/066,094

; PRIOR FILING DATE: 1997-11-17

; PRIOR APPLICATION NUMBER: US 60/066,100

; PRIOR FILING DATE: 1997-11-17

; PRIOR APPLICATION NUMBER: US 60/066,089

; PRIOR FILING DATE: 1997-11-17

; PRIOR APPLICATION NUMBER: US 60/066,095

; PRIOR FILING DATE: 1997-11-17

; PRIOR APPLICATION NUMBER: US 60/066,090

; PRIOR FILING DATE: 1997-11-17

; NUMBER OF SEQ ID NOS: 611

; SOFTWARE: Patentln Ver. 2.0

; SEQ ID NO 139

; LENGTH: 182

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-974-879-139

Query Match 16.6%; Score 26; DB 9; Length 182;

Best Local Similarity 30.8%; Pred. No. 1.1e+03;

Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGC 29

Db 153 PTLVLSACLGIC 165

Search completed: March 27, 2003, 11:03:15

Job time : 14 secs

GenCore version 5.1.4-p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 27, 2003, 10:58:19 ; Search time 44 Seconds

(without alignments)  
211.933 Million cell updates/sec

Title: US-09-828-607-6

Perfect score: 157  
Sequence: 1 XXXXXXXXXXXXXXXXXXXXXXXXXX.....XXXXXXXXXXXXXXXXXXXXCXCX 97

Scoring table:

BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283224 segs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

PIR.73:\*  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	17.2	967	2	G86229 hypothetical prote
2	26	16.6	119	2	S48192 insulin-like growt
3	26	16.6	278	2	T20478 hypothetical prote
4	26	16.6	347	2	T24528 hypothetical prote
5	26	16.6	360	2	I53032 bone morphogenetic
6	26	16.6	470	2	B83991 glycolate oxidase
7	26	16.6	472	1	BMH03 bone morphogenetic
8	26	16.6	476	2	JC4646 bone morphogenetic
9	26	16.6	478	2	JC4838 bone morphogenetic
10	26	16.6	598	2	T02795 probable membrane
11	25	15.9	99	2	S22351 P-glycoprotein - r
12	25	15.9	112	2	A61439 transforming growt
13	25	15.9	240	2	T45814 hypothetical prote
14	25	15.9	366	2	T03907 TGF-beta-related p
15	25	15.9	407	2	H84920 probable Tnf fami
16	25	15.9	407	2	T37242 transforming growt
17	25	15.9	412	2	A39489 transforming growt
18	25	15.9	413	1	WFXLR2 transforming growt
19	25	15.9	414	1	WFMKB2 transforming growt
20	25	15.9	414	1	WFMKB2 transforming growt
21	25	15.9	414	1	A31249 transforming growt
22	25	15.9	442	2	B31249 transforming growt
23	25	15.9	470	2	D69884 transforming growt
24	25	15.9	553	1	A42459 glycolate oxidase
25	25	15.9	553	1	A42459 glycolate oxidase
26	25	15.9	553	1	S20100 mullerian inhibiti
27	25	15.9	563	2	T20192 mullerian inhibiti
28	25	15.9	575	1	WFBOM mullerian inhibiti
29	25	15.9	612	2	G83307 hypothetical prote

#### ALIGNMENTS

##### RESULT 1

G86229

hypothetical protein [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001

C:Accession: G86229

R:Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luro, J.S.; Malt, R.; Marzla

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MID:21016719; PMID:11130712

A:Accession: G86229

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-967 <STO>

A:Cross-references: GB:AE005172; NID:g3482933; PIDN:AAC33218.1; GSPDB:GN00141

C:Genetics:

A:Map position: 1

Query Match

Best Local Similarity 17.2% Score 27; DB 2; Length 967;

Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXCXC 29

DB 726 PQETRRSRCSGAC 738

##### RESULT 2

S48192

insulin-like growth factor S11 precursor - soybean

N:Alternate names: leginsulin

C:Species: Glycine max (soybean)

C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Oct-2000

C:Accession: S48192; PNO116

R:Matanabe, Y.; Barbashov, S.F.; Komatsu, S.; Hemmings, A.M.; Miyagi, M.; Tsunasawa,

Eur. J. Biochem. 224, 167-172, 1994

A:Title: A peptide that stimulates phosphorylation of the plant insulin-binding prote

A:Reference number: S48192; MID:94357216; PMID:8076638

A:Accession: S48192

A:Molecule type: mRNA; protein

A:Residues: 1-119 <WAT>

A:Cross-references: GB:D17996; NID:g498167; PIDN:BAA04219.1; PTD:g498168

Mol. Biol. (Mosk.) 24, 953-961, 1990

A:Title: Using monoclonal antibodies to insulin for isolating proteins inhibiting cel

A:Reference number: PN0115; MUID:91066897; PMID:2250683

A:Accession: PN0116

A:Molecule type: protein

A:Residues: 20-30, 'W', '32-39 <BAR>

F:1-19/Domain: propeptide #status predicted <PRO>

F:20-56/Product: insulin-like growth factor sII #status experimental <MAT>

Query Match 16.6%; Score 26; DB 2; Length 119;

Best Local Similarity 30.8%; Pred. No. 6.9e+02;

Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29

DB 14 PTKIEADKNGAC 26

#### RESULT 3

T20478 hypothetical protein F01G10.6 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C:Accession: T20478

R:Hemby, C.

submitted to the EMBL Data Library, October 1996

A:Reference number: Z19280

A:Accession: T20478

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-278 <MIL>

A:Cross-references: EMBL:Z81055; PIDN:CAB02894.1; GSPDB:GN00022; CESP:F01G10.6

C:Experimental source: clone F01G10

C:Genetics:

A:Gene: CESP:F01G10.6

A:Map position: 4

A:Inserts: 84/1; 168/1

Query Match 16.6%; Score 26; DB 2; Length 278;

Best Local Similarity 30.8%; Pred. No. 1.2e+03;

Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29

DB 59 PSMTFAESCSPC 71

#### RESULT 4

T24528 hypothetical protein T05E12.1 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C:Accession: T24528

R:McMurray, A.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z19904

A:Accession: T24528

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-347 <MIL>

A:Cross-references: EMBL:Z81585; PIDN:CAB04681.1; GSPDB:GN00023; CESP:T05E12.1

C:Experimental source: clone T05E12

C:Genetics:

A:Gene: CESP:T05E12.1

A:Map position: 5

A:Inserts: 61/3; 90/1; 165/2; 187/3; 256/3

QY 17 PXXXXXXCXGXC 29

DB 87 PLIATSGCFCGLC 99

Query Match 16.6%; Score 26; DB 2; Length 347;

Best Local Similarity 30.8%; Pred. No. 1.3e+03;

Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

#### RESULT 5

I53032 bone morphogenetic protein 3 - rat (fragment)

C:Species: *Rattus sp.* (rat)

C>Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 16-Jul-1999

C:Accession: I53032

R:Chen, D.; Feng, J.Q.; Feng, M.; Harris, M.A.; Mahy, P.; Mundy, G.R.; Harris, S.E.

DNA Cell Biol. 14, 235-239, 1995

A:Title: Sequence and expression of bone morphogenetic protein 3 mRNA in prolonged cu

A:Reference number: I53032; MUID:95186061; PMID:7860444

A:Accession: I53032

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Cross-references: GB:S77492; NID:9957225; PIDN:AAB33725.1; PID:9957226

C:Superfamily: Inhibin

Query Match 16.6%; Score 26; DB 2; Length 360;

Best Local Similarity 30.8%; Pred. No. 1.4e+03;

Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29

DB 279 PKSFDAHYCAGC 291

#### RESULT 6

B83991 glycolate oxidase subunit BH2730 [imported] - *Bacillus halodurans* (strain C-125)

C:Species: *Bacillus halodurans*

C>Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001

C:Accession: B83991

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H

Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* a

A:Reference number: B83991; MUID:2051582; PMID:11058132

A:Accession: B83991

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-470 <STO>

A:Cross-references: GB:AP001516; GB:BA000004; NID:910175192; PIDN:BA06449.1; GSPDB:G

C:Experimental source: strain C-125

C:Genetics:

A:Gene: BH2730

C:Superfamily: glycolate oxidase chain glycd

Query Match 16.6%; Score 26; DB 2; Length 470;

Best Local Similarity 30.8%; Pred. No. 1.6e+03;

Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29

DB 69 PRSGTNLCAGTC 81

#### RESULT 7

BHMU3 bone morphogenetic protein 3 precursor - human

N:Alternate names: osteogenin

C:Species: *Homo sapiens* (man)

C>Date: 16-Sep-1992 #sequence\_revision 03-Aug-1995 #text\_change 18-Jun-1999

C:Accession: D37278

R:Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mltsock, L.M.; Whitters, M.J.; Kitz, R.W.;

Science 242, 1528-1534, 1988

A:Title: Novel regulators of bone formation: molecular clones and activities.

A:Reference number: A37278; MUID:89072730; PMID:3201241

A:Accession: D37278

A:Molecule type: mRNA

A:Residues: 1-472 <WO4>

A:Cross-references: GB:M22491; NID:9179505; PIDN:AAA51836.1; PID:9179506

C:Genetics:

A:Gene: GDB:BMF3



A:Cross-references: GDB:125206; OMIM:112263  
 A:Map position: 4p14-4q21  
 C:Superfamily: Inhibin  
 C:Keywords: bone; glycoprotein  
 F:1-22/Domain: signal sequence #status predicted <SIG>  
 F:23-345/Domain: propeptide #status predicted <PRO>  
 F:346-472/Product: bone morphogenetic protein 3 #status predicted <MAT>  
 F:117,141,175,220,463/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 16.6%; Score 26; DB 1; Length 472;  
 Best Local Similarity 30.8%; Pred. No. 1.6e+03;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29  
 DB 391 PKSFDAVYCGAC 403

## RESULT 8

bone morphogenetic protein-3b precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 10-May-1996 #sequence\_revision 19-Jul-1996 #text\_change 01-Dec-2000  
 C:Accession: J04646

R:Takao, M.; Hino, J.; Takeshita, N.; Konno, Y.; Nishizawa, T.; Matsuo, H.; Kangawa, K.  
 Biochem. Biophys. Res. Commun. 219, 656-662, 1996  
 A:Title: Identification of rat bone morphogenetic protein-3b (BMP-3b), a new member of B  
 A:Reference number: J04646; MUID:96133707; PMID:8605043  
 A:Accession: J04646

A:Molecule type: mRNA  
 A:Residues: 1-476 <TAK>  
 A:Cross-references: DDBJ:DA9494; NID:9699625; PIDN:BA08454.1; PID:9699626  
 A:Experimental source: femur

A:Comment: This protein plays a role in the central nervous system as well as in new bon  
 acellular matrix.

C:Superfamily: Inhibin  
 C:Keywords: bone; glycoprotein  
 F:1-29/Domain: signal sequence #status predicted <SIG>  
 F:30-366/Domain: propeptide #status predicted <PRO>  
 F:367-476/Product: bone morphogenetic protein-3b #status predicted <MAT>  
 F:114,152,277,467/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 16.6%; Score 26; DB 2; Length 476;  
 Best Local Similarity 30.8%; Pred. No. 1.6e+03;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29  
 DB 395 PKSFDAVYCGAC 407

## RESULT 9

bone morphogenetic protein-3b precursor [similarity] - human  
 C:Species: Homo sapiens (man)  
 C>Date: 15-Aug-1996 #sequence\_revision 15-Oct-1996 #text\_change 01-Dec-2000  
 C:Accession: J04838

R:Hino, J.; Takao, M.; Takeshita, N.; Konno, Y.; Nishizawa, T.; Matsuo, H.; Kangawa, K.  
 Biochem. Biophys. Res. Commun. 223, 304-310, 1996  
 A:Title: cDNA cloning and genomic structure of human bone morphogenetic protein-3b (BMP-  
 A:Reference number: J04838; MUID:96264636; PMID:8670277  
 A:Accession: J04838

A:Molecule type: mRNA  
 A:Residues: 1-478 <HIN>

A:Cross-references: DDBJ:DA9492; NID:9699603; PIDN:BA08452.1; PID:9699604  
 C:Comment: This protein induces endochondral bone formation, chemotaxis of monocytes, an  
 C:Genetics:  
 A:Gene: bmp-3b  
 C:Superfamily: Inhibin  
 C:Keywords: bone

F:1-33/Domain: signal sequence #status predicted <SIG>

F:34-368/Domain: propeptide #status predicted <PRO>  
 F:369-478/Product: bone morphogenetic protein-3b #status predicted <MAT>

Query Match 16.6%; Score 26; DB 2; Length 478;  
 Best Local Similarity 30.8%; Pred. No. 1.6e+03;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29  
 DB 397 PKSFDAVYCGAC 409

## RESULT 10

probable membrane protein L549.7 [Imported] - Leishmania major (strain Friedlin)  
 C:Species: Leishmania major  
 C>Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 19-May-2000  
 C:Accession: G81455; T02795

R:Myler, P.D.; Audleman, L.; deVos, T.; Hixson, G.; Kiser, P.; Lemley, C.; Magness, C  
 Proc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999  
 A:Title: Leishmania major Friedlin chromosome 1 has an unusual distribution of protel  
 A:Reference number: A81455; MUID:99178987; PMID:10077609  
 A:Accession: G81455

A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-598 <PYL>  
 A:Cross-references: GB:AE001274; NID:93264850; PIDN:AC24619.1; PID:92978456; GSPDB:C  
 A:Experimental source: strain MNOM/IL/81/Friedlin

C:Genetics:  
 A:Gene: L549.7  
 A:Map position: 1  
 C:Superfamily: Leishmania major probable membrane protein L549.7  
 C:Keywords: transmembrane protein

Query Match 16.6%; Score 26; DB 2; Length 598;  
 Best Local Similarity 30.8%; Pred. No. 1.9e+03;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29  
 DB 96 PSSSSSGCGCGC 108

## RESULT 11

P-glycoprotein - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 05-Nov-1999  
 C:Accession: S22351

R:Deuchars, K.L.; Duttle, M.; Ling, V.  
 Biochim. Biophys. Acta 1130, 157-165, 1992  
 A:Title: Identification of distinct P-glycoprotein gene sequences in rat.  
 A:Reference number: S22351; MUID:92223089; PMID:1348630  
 A:Accession: S22351

A:Molecule type: DNA  
 A:Residues: 1-99 <DEU>  
 A:Cross-references: EMBL:X61106; NID:956800; PIDN:CAA43418.1; PID:e39738; PID:g133421  
 A>Note: the authors translated the codon TTC for residue 48 as Leu  
 A>Note: the authors did not translate the codon for residue 99  
 C:Keywords: glycoprotein

Query Match 15.9%; Score 25; DB 2; Length 99;  
 Best Local Similarity 30.8%; Pred. No. 8.8e+02;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29  
 DB 42 PSVTALFLCFGR 54

## RESULT 12

A61439  
 transforming growth factor beta-2 - bovine

N:Alternate names: cartilage-inducing factor B; MGF-a; milk growth factor a  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-May-1999  
 C:Accession: A61439; A25485; B42320; S15389  
 R:Jin, Y.; Cox, D.A.; Knecht, R.; Raschdorf, F.; Cerretti, N.  
 J. Protein Chem. 10, 565-575, 1991  
 A:Title: Separation, purification, and sequence identification of TGF-beta1 and TGF-beta  
 A:Reference number: A61439; PMID:92189724; PMID:1799413  
 A:Accession: A61439  
 A:Molecule type: protein  
 A:Residues: 1-112 <JIN>  
 A:Experimental source: milk  
 R:Sejdel, S.M.; Segarini, P.R.; Rosen, D.M.; Thompson, A.V.; Bentz, H.; Graycar, J.  
 J. Biol. Chem. 262, 1946-1949, 1987  
 A:Title: Cartilage-inducing factor-B is a unique protein structurally and functionally  
 A:Reference number: A25485; PMID:87137406; PMID:3469199  
 A:Accession: A25485  
 A:Molecule type: protein  
 A:Residues: 1-30 <SEY>  
 A:Experimental source: bone  
 R:Ogawa, Y.; Schmidt, D.K.; Dasch, J.R.; Chang, R.J.; Glaser, C.B.  
 J. Biol. Chem. 267, 2325-2328, 1992  
 A:Title: Purification and characterization of transforming growth factor-beta2.3 and -b  
 A:Reference number: A42320; PMID:92129307; PMID:1733936  
 A:Accession: B42320  
 A:Molecule type: protein  
 A:Residues: 1-6, 'X', 8-14, 'XX', 17-34 <OGA>  
 A:Experimental source: bone  
 R:Cox, D.A.; Buerk, R.R.  
 Eur. J. Biochem. 197, 353-358, 1991  
 A:Title: Isolation and characterization of milk growth factor, a transforming growth fac  
 A:Reference number: S15389; PMID:91224126; PMID:2026157  
 A:Accession: S15389  
 A:Molecule type: protein  
 A:Residues: 1-16, 'XX', 19 <COX>  
 A:Experimental source: milk  
 C:Superfamily: Inhibin  
 C:Keywords: growth factor; growth regulation; heterodimer; homodimer

Query Match 15.9%; Score 25; DB 2; Length 112;  
 Best Local Similarity 30.8%; Pred. No. 9.6e+02;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29  
 DB 36 PKGYNNFCAGAC 48

RESULT 13  
 T45814  
 hypothetical protein F2809.210 - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 04-Feb-2000  
 C:Accession: T45814  
 R:Benes, V.; Rechmann, S.; Borkova, D.; Ansoerge, W.; Meves, H.W.; Lemcke, K.; Mayer, K.F.  
 submitted to the Protein Sequence Database, January 2000  
 A:Reference number: Z23014  
 A:Accession: T45814  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-240 <BEN>  
 A:Cross-references: EMBL:AL137080  
 A:Experimental source: cultivar Columbia; BAC clone F2809  
 C:Genetics:  
 A:Map position: 3  
 A:Introns: 38/2; 82/2; 123/2; 196/2  
 A:Note: F2809.210

Query Match 15.9%; Score 25; DB 2; Length 240;  
 Best Local Similarity 30.8%; Pred. No. 1.5e+03;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29

DB 136 PGEESACAGEC 148

RESULT 14  
 T03907  
 TGF-beta-related protein homolog F3963.8 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 17-Mar-2000  
 C:Accession: T03907  
 R:Du, Z.; Le, T.T.; Holmes, A.  
 submitted to the EMBL Data Library, July 1997  
 A:Description: The sequence of C. elegans cosmid F3963.  
 A:Reference number: Z15131  
 A:Accession: T03907  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-366 <DUZ>  
 A:Cross-references: EMBL:AF016424; NID:q2291203; PIDN:AB65333.1; PID:q2291211  
 C:Genetics:  
 A:Map position: V  
 A:Introns: 38/2; 86/2; 110/1; 161/2; 205/1; 229/2; 259/1  
 A:Note: F3963.8  
 C:Superfamily: Inhibin

Query Match 15.9%; Score 25; DB 2; Length 366;  
 Best Local Similarity 30.8%; Pred. No. 2e+03;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29  
 DB 286 PEGSAPYCSGDC 298

RESULT 15  
 H84920  
 probable Tubb family protein [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
 C:Accession: H84920  
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bentto, M.I.; Town, C.D.; Fujii, C.Y.  
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,  
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter  
 Nature 402, 761-768, 1999  
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
 A:Reference number: A84420; PMID:20083487; PMID:10617197  
 A:Accession: H84920  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-407 <STO>  
 A:Cross-references: GB:AE002093; NID:g3738302; PIDN:AAC63644.1; GSPDB:GN00139  
 C:Genetics:  
 A:Gene: At2g47900  
 A:Map position: 2

Query Match 15.9%; Score 25; DB 2; Length 407;  
 Best Local Similarity 30.8%; Pred. No. 2.1e+03;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29  
 DB 75 PSRRNVSCAGVC 87

Search completed: March 27, 2003, 11:02:33  
 Job time : 45 secs



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CC EMBL; AF042381; AAC38334.1; -  
 DR EMBL; AE013388; AAM31239.1; -  
 DR TIGRAME; TIGR01111; mtrA; 1.  
 KW transferase; Methyltransferase; Methanogenesis; Cobalt.  
 FT BINDING 85 85  
 FT  
 FT DOMAIN 169 176  
 FT POLY-GLUT.  
 FT DOMAIN 232 238  
 FT POLY-LEU.  
 FT CONFLICT 16 16 G -> R (IN REF. 1).  
 FT CONFLICT 71 71 N -> D (IN REF. 1).  
 FT CONFLICT 127 127 E -> G (IN REF. 1).  
 FT CONFLICT 161 161 D -> E (IN REF. 1).  
 SQ SEQUENCE 240 AA; 25366 MW; 44C086DD3561E526 CRC64;

Query Match 17.2%; Score 27; DB 1; Length 240;  
 Best Local Similarity 30.8%; Pred. No. 2.3e+02;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 17 PXXXXXXCXGXC 29  
 DB 40 PILDAGAACTGSC 52

RESULT 2  
 ID ALBI\_GLYSO STANDARD; PRT; 119 AA.  
 AC 0920X0;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Albumin 1 precursor (PA1) [contains: PA1a; Leginsulin (PA1B)].  
 OS Glycine soja.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC Eurosidia I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
 NX NCBI\_TaxID=3848;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Tan J.Z., Lou C.F., Hirano H.;  
 RT "Analysis of leginsulin gene in soybean cultivar (Glycine max) and  
 RT wild species (Glycine soja).";  
 RL Chin. J. Appl. Environ. Biol. 5:259-263(1999).  
 CC -1- FUNCTION: LEGINSULIN BINDS TO BASIC 7S GLOBULIN (BG) AND  
 CC STIMULATES ITS PHOSPHORYLATION ACTIVITY (BY SIMILARITY).  
 CC -1- PTM: THREE DISULFIDE BONDS ARE PROBABLY PRESENT.  
 CC -1- PTM: THE C-TERMINAL GLYCINE MAY BE REMOVED FROM LEGINSULIN.  
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DR EMBL; AJ011935; CAA09880.2; -  
 KW Seed storage protein; Albumin; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 56 LEGINSULIN (BY SIMILARITY).  
 FT PROPEP 57 64 POTENTIAL.  
 FT CHAIN 65 117 PA1A (POTENTIAL).  
 FT PROPEP 118 119 POTENTIAL.  
 SQ SEQUENCE 119 AA; 12963 MW; EE5457D8D09070CC CRC64;

Query Match 16.6%; Score 26; DB 1; Length 119;  
 Best Local Similarity 30.8%; Pred. No. 2.1e+02;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 17 PXXXXXXCXGXC 29

DB 14 PTKIEADNCAGC 26

RESULT 3  
 ID ALBI\_SOYBN STANDARD; PRT; 119 AA.  
 AC 039837; O49854;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Albumin 1 precursor (PA1) [contains: PA1a; Leginsulin (PA1B)].  
 OS Glycine max (Soybean).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC Eurosidia I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
 NX NCBI\_TaxID=3847;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN-cv. Miyagishihrome; TISSUE-Radicle;  
 RX MEDLINE=94357216; PubMed=8076638;  
 RA Watanabe Y., Barbashov S.F., Komatsu S., Hemmings A.M., Miyagi M.,  
 RA Tsunashima S., Hirano H.,  
 RT "A peptide that stimulates phosphorylation of the plant insulin-  
 RT binding protein. Isolation, primary structure and cDNA cloning.";  
 RL Eur. J. Biochem. 224:167-172(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN-cv. Miyagishihrome;  
 RA Tan J.Z., Lou C.F., Hirano H.;  
 RT "Analysis of leginsulin gene in soybean cultivar (Glycine max) and  
 RT wild species (Glycine soja).";  
 RL Chin. J. Appl. Environ. Biol. 5:259-263(1999).  
 RN [3]  
 RP REVISION TO 64.  
 RA STRAIN-cv. Miyagishihrome;  
 RA Hirano H.;  
 RL Submitted (JUN-2001) to the SWISS-PROT data bank.  
 CC -1- FUNCTION: LEGINSULIN BINDS TO BASIC 7S GLOBULIN (BG) AND  
 CC STIMULATES ITS PHOSPHORYLATION ACTIVITY. INVOLVED IN THE SIGNAL  
 CC TRANSDUCTION SYSTEM TO REGULATE THE GROWTH AND DIFFERENTIATION AS  
 CC A HORMONE PEPTIDE.  
 CC -1- PTM: THREE DISULFIDE BONDS ARE PROBABLY PRESENT IN LEGINSULIN.  
 CC -1- PTM: THE C-TERMINAL GLYCINE MAY BE REMOVED FROM LEGINSULIN.  
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DR EMBL; D17396; BAA04219.1; -  
 KW Seed storage protein; Albumin; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 56 LEGINSULIN.  
 FT PROPEP 57 64 POTENTIAL.  
 FT CHAIN 65 116 PA1A (POTENTIAL).  
 FT PROPEP 117 119 POTENTIAL.  
 SQ SEQUENCE 119 AA; 13046 MW; A054491D7B1AA70 CRC64;

Query Match 16.6%; Score 26; DB 1; Length 119;  
 Best Local Similarity 30.8%; Pred. No. 2.1e+02;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 17 PXXXXXXCXGXC 29  
 DB 14 PTKIEADNCAGC 26

RESULT 4

1816\_DROME STANDARD; PRT; 355 AA.  
 ID 1816\_DROME  
 AC 09VAR0;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical protein CG7816.  
 GN CG7816.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 NC NCBL\_taxid=7227;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RC STRAIN=Berkeley;  
 RP SEQUENCE FROM N.A.  
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Aghayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,  
 RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,  
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin R.K., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Fjosek A., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Foster C., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagham C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.Y., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,  
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Sytkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster."  
 RL Science 287:2185-2195(2000).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).  
 CC -1- SIMILARITY: BELONGS TO THE KIF4/CATSPF FAMILY.  
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FT TRANSMEM 118 138 POTENTIAL.  
 FT TRANSMEM 273 293 POTENTIAL.  
 FT TRANSMEM 301 321 POTENTIAL.  
 FT CAROHD 4 4 N-LINKED (GLCNAc... ) (POTENTIAL).  
 FT CAROHD 218 218 N-LINKED (GLCNAc... ) (POTENTIAL).  
 SQ SEQUENCE 355 AA; 38870 MW; 01527C0390741FE8 CRC64;  
 Query Match 16.6%; Score 26; DB 1; Length 355;  
 Best Local Similarity 30.8%; Pred. No. 4.4e+02;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 QY 17 PXXXXXXCXKC 29  
 DB 165 PEGETSESCGAC 177  
 RESULT 5  
 ID BMP3\_RAT STANDARD; PRT; 468 AA.  
 AC P49002;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Bone morphogenetic protein 3 precursor (BMP-3).  
 GN BMP3 OR BMP-3.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NC NCBL\_Taxid=10116;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Calvaria;  
 RA Takeo M., Hino J., Kangawa K., Matsuo H.;  
 RL Submitted (Aug-1995) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 109-468 FROM N.A.  
 RC TISSUE=Calvaria;  
 RX MEDLINE=95186061; PubMed=7880444;  
 RA Chen D., Feng J.Q., Feng M., Harris M.A., Mahy P., Mundy G.R.,  
 RA Harris S.E.;  
 RT "Sequence and expression of bone morphogenetic protein 3 mRNA in  
 RT prolonged cultures of fetal rat calvarial osteoblasts and in rat  
 RT prostate adenocarcinoma PA III cells."  
 RL DNA Cell Biol. 14:235-239(1995).  
 CC -1- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.  
 CC -1- SUBUNIT: HOMODIMER: DISULFIDE-LINKED (BY SIMILARITY).  
 CC -1- TISSUE SPECIFICITY: HIGH LEVELS IN TRACHEA, SPLEEN, SMALL  
 CC INTESTINE, AND OVARY, AND AT LOW LEVELS IN CEREBELLUM, COSTA AND  
 CC BONE MARROW.  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
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EMBL: D63860; BA09922.1; -;  
 EMBL: S77492; AB33725.1; -;  
 DR HSSP: P12643; 3BMP.  
 DR InterPro: IPR002400; GF\_cysknob.  
 DR InterPro: IPR001839; TGFb.  
 DR Pfam: PF00019; TGF-beta.1.  
 DR PRINTS: PR00438; GFCSKNOT.  
 DR PRODOM: P000357; TGFb.1.  
 DR SMART: SM00204; TGFb.1.  
 DR PROSITE: PS00250; TGF\_BETA.1; 1.  
 KW Signal: Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.  
 FT SIGNAL 1 22 POTENTIAL.  
 FT PROPEP 23 358 POTENTIAL.  
 FT CHAIN 359 468 BONE MORPHOGENETIC PROTEIN 3.

FT DISULFID 366 433 BY SIMILARITY.  
 FT DISULFID 395 465 BY SIMILARITY.  
 FT DISULFID 399 467 BY SIMILARITY.  
 FT DISULFID 432 432 INTERCHAIN (BY SIMILARITY).  
 FT CARBOHYD 115 115 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 216 216 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 468 AA; 52675 MW; 05315D4954DC3C64; CRC64;

Query Match 16.6%; Score 26; DB 1; Length 468;  
 Best Local Similarity 30.8%; Pred. No. 5.3e+02;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 17 PXXXXXXCXGXC 29  
 DB 387 PKSFDAVYCSGAC 399

## RESULT 6

BMP3\_HUMAN STANDARD; PRT; 472 AA.

AC P12645; 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Bone morphogenetic protein 3 precursor (BMP-3) (Osteogenin) (BMP-3A).  
 GN BMP3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP MEDLINE=89072730; PubMed=3201241;  
 RA Wozney J.M., Rosen V., Celeste A.J., Mitscock L.M., Whitters M.J.,  
 RA Kriz R.W., Hewick R.M., Wang E.A.;  
 RT "Novel regulators of bone formation: molecular clones and  
 RT activities.";  
 RL Science 242:1528-1534(1988).  
 CC -1- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.  
 CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LUNG, OVARY AND SMALL INTESTINE.  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
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 CC -----  
 CC EMBL: M22491; AAA51836.1; -  
 CC PIR: D37278; D37278.  
 DR HSSP: P12643; 3BMP.  
 DR Genew: HGNC:1070; BMP3.  
 DR MIM: 112263; -  
 DR InterPro: IPR002400; GF\_cysknot.  
 DR InterPro: IPR001839; TGFb.  
 DR Pfam: PF00019; TGF-beta.1.  
 DR PRINTS: PR00438; GFCYSKNOT.  
 DR Prodom: PD000357; TGFb.1.  
 DR SMART: SM00204; TGFb.1.  
 DR PROSITE: PS00250; TGF\_BETA\_1; 1.  
 KW Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.  
 FT SIGNAL 1  
 FT CHAIN 23 362 POTENTIAL.  
 FT PROPEP 23 362 POTENTIAL.  
 FT CHAIN 363 472 BONE MORPHOGENETIC PROTEIN 3.  
 FT DISULFID 370 437 BY SIMILARITY.  
 FT DISULFID 399 469 BY SIMILARITY.  
 FT DISULFID 403 471 BY SIMILARITY.

FT DISULFID 436 436 INTERCHAIN (BY SIMILARITY).  
 FT CARBOHYD 117 117 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 175 175 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 220 220 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 472 AA; 53406 MW; 95C3B7BD5C9D596F CRC64;

Query Match 16.6%; Score 26; DB 1; Length 472;  
 Best Local Similarity 30.8%; Pred. No. 5.4e+02;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 17 PXXXXXXCXGXC 29  
 DB 391 PKSFDAVYCSGAC 403

## RESULT 7

BMP3\_MOUSE STANDARD; PRT; 476 AA.

AC P9737; 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Bone morphogenetic protein 3b precursor (BMP-3b)  
 DE (Growth/differentiation factor 10) (GDF-10).  
 GN GDF10 OR BMP3B.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.  
 RC STRAIN=CD-1; TISSUE=Uterus;  
 RX MEDLINE=96115614; PubMed=8679252;  
 RA Cunningham N.S., Jenkins N.A., Gilbert D.J., Copeland N.G.,  
 RA Reddi A.H., Lee S.-J.;  
 RT "Growth/differentiation factor-10: a new member of the transforming  
 RT growth factor-beta superfamily related to bone morphogenetic  
 RT protein-3.";  
 RL Growth Factors 12:99-109(1995).  
 CC -1- SUBUNIT: HOMODIMER OR HETERODIMER (POTENTIAL).  
 CC -1- TISSUE SPECIFICITY: Expressed in uterus, adipose tissue, brain and  
 CC bone, and to a lesser extent in liver and spleen.  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
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 CC -----  
 CC EMBL: S82648; AAB46753.1; -  
 CC HSSP: P12643; 3BMP.  
 DR MGD: MGI:95684; Gdf10.  
 DR InterPro: IPR001839; TGFb.  
 DR Pfam: PF00019; TGF-beta.1.  
 DR Prodom: PD000357; TGFb.1.  
 DR SMART: SM00204; TGFb.1.  
 DR PROSITE: PS00250; TGF\_BETA\_1; 1.  
 KW Signal; Growth factor; Cytokine; glycoprotein.  
 FT SIGNAL 1  
 FT PROPEP 30 366 POTENTIAL.  
 FT CHAIN 367 476 POTENTIAL.  
 FT DISULFID 374 441 BY SIMILARITY.  
 FT DISULFID 403 473 BY SIMILARITY.  
 FT DISULFID 440 475 BY SIMILARITY.  
 FT DISULFID 440 440 INTERCHAIN (BY SIMILARITY).  
 FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 467 467 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 476 AA; 52490 MW; 15D4CB86540FE82 CRC64;

Query Match  
Best Local Similarity 30.8%; Score 26; DB 1; Length 476;  
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29  
DB 395 PKSFAYYCAGAC 407

## RESULT 8

BM3B\_HUMAN STANDARD; PRT; 476 AA.  
ID BM3B\_HUMAN  
AC P55108;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Bone morphogenetic protein 3b precursor (BMP-3b)  
DE (Growth/differentiation factor 10) (GDF-10) (Bone inducing protein)  
DE (BIP).  
GN GDF10 OR BMP3B.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Rattus.  
OX NCBI\_Taxid=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC SPRATN-Sprague-Dawley; TISSUE=Femur;  
RX MEDLINE=96193707; PubMed=8605043;  
RA Takao M., Hino J., Takeshita N., Konno Y., Nishizawa T.,  
RA Matsuo H., Kangawa K.;  
RT "Identification of rat bone morphogenetic protein-3b (BMP-3b), a new  
member of BMP-3.";  
RT Biochem. Biophys. Res. Commun. 219:656-662(1996).  
RT  
CC -1- SUBUNIT: HOMODIMER OR HETERODIMER (POTENTIAL).  
CC -1- TISSUE SPECIFICITY: COSTA, COSTICARTILAGE, FEMUR, CALVARIA,  
TRACHEA, AORTA AND BRAIN. PREDOMINANTLY IN THE CEREBELLUM.  
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
CC  
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CC  
CC EMBL: D49494; BAA08454.1; -.  
DR HSSP: P12643; 3BMP.  
DR InterPro: IPR001839; TGF-beta.  
DR Pfam: PF00019; TGF-beta; 1.  
DR ProDom: PD000357; TGF-beta; 1.  
DR SMART: SM00204; TGF-beta; 1.  
DR PROSITE: PS00250; TGF-BETA\_1; 1.  
KW Signal; Growth factor; Cytokine; Glycoprotein.  
FT SIGNAL 1  
FT PROPEP 30  
FT CHAIN 367  
FT DISULFID 374  
FT DISULFID 403  
FT DISULFID 407  
FT DISULFID 475  
FT DISULFID 475  
FT DISULFID 475  
FT DISULFID 475  
FT CARBOHYD 114  
FT CARBOHYD 114  
FT CARBOHYD 152  
FT CARBOHYD 152  
FT CARBOHYD 277  
FT CARBOHYD 277  
SQ SEQUENCE 476 AA; 52960 MW; 873F4D4150C625EE CRC64;

Query Match  
Best Local Similarity 30.8%; Score 26; DB 1; Length 476;  
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29  
DB 395 PKSFAYYCAGAC 407

## RESULT 9

BM3B\_HUMAN STANDARD; PRT; 478 AA.  
ID BM3B\_HUMAN  
AC P55107; G9UCX6;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Bone morphogenetic protein 3b precursor (BMP-3b)  
DE (Growth/differentiation factor 10) (GDF-10) (Bone inducing protein)  
DE (BIP).  
GN GDF10 OR BMP3B.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Femur;  
RX MEDLINE=96264636; PubMed=8670277;  
RA Hino J., Takao M., Takeshita N., Konno Y., Nishizawa T.,  
RA Matsuo H., Kangawa K.;  
RT "CDNA cloning and genomic structure of human bone morphogenetic  
protein-3b (BMP-3b)."  
RT Biochem. Biophys. Res. Commun. 223:304-310(1996).  
RN [2]  
RP SEQUENCE OF 360-478 FROM N.A.  
RC TISSUE=uterus;  
RX MEDLINE=96115614; PubMed=8679252;  
RA Cunningham N.S., Jenkins N.A., Gilbert D.J., Copeland N.G.,  
RA Reddi A.H., Lee S.J.;  
RT "Growth/differentiation factor-10: a new member of the transforming  
growth factor-beta superfamily related to bone morphogenetic protein-  
3.";  
RT Growth Factors 12:99-109(1995).  
RT  
CC -1- SUBUNIT: HOMODIMER OR HETERODIMER (POTENTIAL).  
CC -1- TISSUE SPECIFICITY: FEMUR, BRAIN, LUNG, SKELETAL MUSCLE, PANCREAS  
AND TESTIS.  
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
CC  
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CC  
CC EMBL: D49493; BAA08453.1; -.  
DR HSSP: P12643; 3BMP.  
DR InterPro: IPR001839; TGF-beta.  
DR Pfam: PF00019; TGF-beta; 1.  
DR ProDom: PD000357; TGF-beta; 1.  
DR SMART: SM00204; TGF-beta; 1.  
DR PROSITE: PS00250; TGF-BETA\_1; 1.  
KW Signal; Growth factor; Cytokine; Glycoprotein.  
FT SIGNAL 1  
FT PROPEP 34  
FT CHAIN 369  
FT DISULFID 376  
FT DISULFID 405  
FT DISULFID 409  
FT DISULFID 442  
FT DISULFID 442  
FT CARBOHYD 118  
FT CARBOHYD 156  
SQ SEQUENCE 478 AA; 52960 MW; 873F4D4150C625EE CRC64;

Query Match  
Best Local Similarity 30.8%; Score 26; DB 1; Length 476;  
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

FT CARBOHYD 281 281 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 469 469 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 478 AA; 53121 MW; 80AE0FA4C50B23A9 CRC64;

Query Match  
 Best Local Similarity 30.8%; Score 26; DB 1; Length 478;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 17 PXXXXXXCXCXC 29  
 DB 397 PKSFAYCAGAC 409

RESULT 10  
 TGF2\_BOVIN  
 ID TGF2\_BOVIN STANDARD; PRT; 112 AA.  
 AC P21214;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Transforming growth factor beta 2 (TGF-beta 2) (Milk growth factor) (MGF).  
 GN TGFβ2.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_Taxid-9913;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE-Milk;  
 RX MEDLINE-92189724; PubMed-1799413;  
 RA Jin Y., Cox D.A., Knecht R., Raschdorf F., Cerletti N.;  
 RT "Separation, purification, and sequence identification of TGF-beta 1  
 and TGF-beta 2 from bovine milk."  
 RL J. Biol. Chem. 10:565-575(1991).  
 RN [2]  
 RP SEQUENCE OF 1-30.  
 RC TISSUE-Bone;  
 RX MEDLINE-87137406; PubMed-3469199;  
 RA Seyedin S.M., Segarini P.R., Rosen D.M., Thompson A.V., Bentz H.,  
 RA Graycar J.;  
 RT "Cartilage-inducing factor-B is a unique protein structurally and  
 RT functionally related to transforming growth factor-beta."  
 RL J. Biol. Chem. 262:1946-1949(1987).  
 RN [3]  
 RP SEQUENCE OF 1-19.  
 RC TISSUE-Milk;  
 RX MEDLINE-91224126; PubMed-2026157;  
 RA Cox D.A., David A., Buett R.R.;  
 RT "Isolation and characterization of milk growth factor, a  
 RT transforming-growth-factor-beta 2-related polypeptide, from bovine  
 RT milk."  
 RL Eur. J. Biochem. 197:353-358(1991).  
 RN [4]  
 RP SUBUNITS.  
 RC TISSUE-Bone;  
 RX MEDLINE-92129307; PubMed-1739336;  
 RA Ogawa Y., Schmidt D.K., Dasch J.R., Chang R.J., Glaser C.B.;  
 RT "Purification and characterization of transforming growth factor-beta  
 RT 2.3 and -beta 1.2 heterodimers from bovine bone."  
 RL J. Biol. Chem. 267:2325-2328(1992).  
 CC -1- FUNCTION: TGF-BETA 2 HAS SUPPRESSIVE EFFECTS ON INTERLEUKIN-2  
 CC DEPENDENT T-CELL GROWTH.  
 CC -1- SUBUNIT: HOMODIMER: DISULFIDE-LINKED. HETERODIMERS OF TGF-BETA 1/2  
 CC AND OF TGF-BETA 2/3 HAVE BEEN FOUND IN BONE.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
 DR PIR: S15389; S15389.  
 DR HSSP: P08112; 2TGI.  
 DR InterPro: IPR002400; GF\_cysknot.  
 DR InterPro: IPR001839; TGFb.  
 DR Pfam: PF00019; TGF-beta; 1.

DR PRINTS: PR00438; GFCYSKNOT.  
 DR PRODOM: PD000357; TGFb; 1.  
 DR SMART: SM00204; TGFb; 1.  
 DR PROSITE: PS00250; TGF-BETA 1; 1.  
 DR Growth factor; Mitogen; Milk.  
 FT DISULFID 7 16 BY SIMILARITY.  
 FT DISULFID 15 78 BY SIMILARITY.  
 FT DISULFID 44 109 BY SIMILARITY.  
 FT DISULFID 48 111 BY SIMILARITY.  
 FT DISULFID 77 77 INTERCHAIN (BY SIMILARITY).  
 SQ SEQUENCE 112 AA; 12719 MW; 5142C74324EBE1C CRC64;

Query Match  
 Best Local Similarity 15.9%; Score 25; DB 1; Length 112;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 17 PXXXXXXCXCXC 29  
 DB 36 PKGYNAFCAGAC 48

RESULT 11  
 BMB8\_MOUSE  
 ID BMB8\_MOUSE STANDARD; PRT; 399 AA.  
 AC P5105;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Bone morphogenetic protein 8B precursor (BMP-8B).  
 GN BMP8B.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid-10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-ICR; TISSUE-Placenta;  
 RX MEDLINE-97000308; PubMed-8843393;  
 RA Zhao G.Q., Hogan B.L.;  
 RT "Evidence that mouse Bmp8a (Op2) and Bmp8b are duplicated genes that  
 RT play a role in spermatogenesis and placental development."  
 RL Mech. Dev. 57:159-168(1996).  
 CC -1- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION. MAY BE THE  
 CC OSTEOINDUCTIVE FACTOR RESPONSIBLE FOR THE PHENOMENON OF  
 CC EPITHELIAL OSTEOGENESIS. PLAYS A ROLE IN CALCIUM REGULATION  
 CC AND BONE HOMEOSTASIS (BY SIMILARITY).  
 CC -1- SUBUNIT: HOMODIMER: DISULFIDE-LINKED.  
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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 CC  
 DR EMBL: U39545; AAB1573.1; -.  
 DR HSSP: P18075; 1BMP.  
 DR MCD: MG1107335; Bmp8b.  
 DR InterPro: IPR002400; GF\_cysknot.  
 DR InterPro: IPR001839; TGFb.  
 DR InterPro: IPR001111; TGFb.N.  
 DR Pfam: PF00019; TGF-beta; 1.  
 DR Pfam: PF00688; TGFb\_propeptide; 1.  
 DR PRINTS: PR00438; GFCYSKNOT.  
 DR PRODOM: PD000357; TGFb; 1.  
 DR SMART: SM00204; TGFb; 1.  
 DR PROSITE: PS00250; TGF-BETA 1; 1.  
 KW Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT PROPEP 20 260



FT CHAIN 261 399 BONE MORPHOGENETIC PROTEIN 8B.  
FT DISULFID 298 364 BY SIMILARITY.  
FT DISULFID 327 396 BY SIMILARITY.  
FT DISULFID 331 398 BY SIMILARITY.  
FT DISULFID 363 363 INTERCHAIN (BY SIMILARITY).  
FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 340 340 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 399 AA; 44752 MW; EFA0B78C7EC4839 CRC64;  
  
Query Match 15.9%; Score 25; DB 1; Length 399;  
Best Local Similarity 30.8%; Pred. No. 6.9e+02;  
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
  
QY 17 PXXXXXXCXKXC 29  
DB 319 PGYSAYCAGEC 331  
  
RESULT 12  
TGF2\_CHICK STANDARD; PRT; 412 AA.  
AC P30371;  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Transforming growth factor beta 2 precursor (TGF-beta 2).  
GN TGFBR2.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=White leghorn; TISSUE=Blood;  
RX MEDLINE=92075163; PubMed=1683775;  
RA Burt D.W., Paton I.R.;  
RT "Molecular cloning and primary structure of the chicken transforming  
growth factor-beta 2 gene."  
RL DNA Cell Biol. 10:723-734(1991).  
CC -1- FUNCTION: TGF-BETA 2 HAS SUPPRESSIVE EFFECTS ON INTERLEUKIN-2  
DEPENDENT T-CELL GROWTH.  
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
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CC  
EMBL: X58071; CAA1101.1; -  
EMBL: X59082; CAA1101.1; JOINED.  
EMBL: X59081; CAA1101.1; JOINED.  
EMBL: X59080; CAA1101.1; JOINED.  
PIR: A39489; A39489.  
DR HSSP: P08112; 2TGI.  
DR InterPro: IPR002400; GF\_cysknot.  
DR InterPro: IPR003911; TGF\_TGFB.  
DR InterPro: IPR001839; TGFB.  
DR InterPro: IPR001111; TGFB\_N.  
DR Pfam: PF000019; TGF-beta; 1.  
DR Pfam: PF00688; TGFB\_propeptide; 1.  
DR PRINTS: PR00438; GFCYSKNOT.  
DR PRINTS: PR01423; TGFETA.  
DR PRODOM: PD000357; TGFB; 1.  
DR SMART: SM00204; TGFB; 1.  
DR PROSITE: PS00250; TGF\_BETA\_1; 1.  
KW Growth factor; Mitogen; Glycoprotein; Signal.  
FT SIGNAL 1 20 POTENTIAL.

FT PROPEP 21 300 TRANSFORMING GROWTH FACTOR BETA 2.  
FT CHAIN 301 412 BY SIMILARITY.  
FT DISULFID 307 412 BY SIMILARITY.  
FT DISULFID 315 378 BY SIMILARITY.  
FT DISULFID 344 409 BY SIMILARITY.  
FT DISULFID 348 411 BY SIMILARITY.  
FT DISULFID 377 377 INTERCHAIN (BY SIMILARITY).  
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 240 240 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 412 AA; 47606 MW; 93E759B71BD958DC CRC64;  
  
Query Match 15.9%; Score 25; DB 1; Length 412;  
Best Local Similarity 30.8%; Pred. No. 7.1e+02;  
Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
  
QY 17 PXXXXXXCXKXC 29  
DB 336 PRGYHANCAGAC 348  
  
RESULT 13  
TGF2\_XENLA STANDARD; PRT; 413 AA.  
ID TGF2\_XENLA  
AC P17247;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Transforming growth factor beta 2 precursor (TGF-beta 2).  
GN TGFBR2.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90245678; PubMed=2336403;  
RA Rebert M.L., Bhatia-Dey N., David I.B.;  
RT "The sequence of TGF-beta 2 from Xenopus laevis."  
RL Nucleic Acids Res. 18:2185-2185(1990).  
CC -1- FUNCTION: TGF-BETA 2 HAS SUPPRESSIVE EFFECTS ON INTERLEUKIN-2  
DEPENDENT T-CELL GROWTH.  
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
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CC  
EMBL: X51817; CAA36116.1; -  
EMBL: X51817; CAA36117.1; ALT\_INT.  
PIR: S09510; S09510.  
DR HSSP: P08112; 2TGI.  
DR InterPro: IPR002400; GF\_cysknot.  
DR InterPro: IPR003911; TGF\_TGFB.  
DR InterPro: IPR001839; TGFB.  
DR InterPro: IPR001111; TGFB\_N.  
DR Pfam: PF000019; TGF-beta; 1.  
DR Pfam: PF00688; TGFB\_propeptide; 1.  
DR PRINTS: PR00438; GFCYSKNOT.  
DR PRINTS: PR01423; TGFETA.  
DR PRODOM: PD000357; TGFB; 1.  
DR SMART: SM00204; TGFB; 1.  
DR PROSITE: PS00250; TGF\_BETA\_1; 1.  
KW Signal; Mitogen; Glycoprotein; Growth factor.  
FT SIGNAL 1 19 POTENTIAL.  
FT PROPEP 20 301

FT CHAIN 302 413 TRANSFORMING GROWTH FACTOR BETA 2.  
 FT DISULFID 308 317 BY SIMILARITY.  
 FT DISULFID 316 379 BY SIMILARITY.  
 FT DISULFID 345 410 BY SIMILARITY.  
 FT DISULFID 349 412 BY SIMILARITY.  
 FT DISULFID 378 378 INTERCHAIN (BY SIMILARITY).  
 FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 413 AA; 47639 MW; 6127715838734010 CRC64;  
 Query Match 15.9%; Score 25; DB 1; Length 413;  
 Best Local Similarity 30.8%; Pred. No. 7.1e+02;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 Oy 17 PXXXXXXCXGXC 29  
 Db 337 PKGYNNFCGAC 349  
 RESULT 14  
 TGF2\_HUMAN STANDARD: PRT: 414 AA.  
 ID TGF2\_HUMAN  
 AC P08112: Q15579; Q15581;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Transforming growth factor beta 2 precursor (TGF-beta 2)  
 DE (Globlastoma-derived T-cell suppressor factor) (G-TSF) (BSC-1 cell  
 DE growth inhibitor) (Polyergin) (Celemin).  
 GN TGF2.  
 OS Homo sapiens (Human), and  
 OS Cercopithecus aethiops (Green monkey) (Griwet).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606, 9534;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM A).  
 RC SPECIES-Human;  
 RX MEDLINE=8811555; PubMed=3322813;  
 RA de Martin R., Haendler B., Hofer-Warbinek R., Gaugitsch H., Wran M.,  
 RA Schueener H., Siefert J.M., Bodner S., Fontana A., Hofer E.;  
 RT "Complementary DNA for human glioblastoma-derived T cell suppressor  
 RT factor," a novel member of the transforming growth factor-beta gene  
 RT family.";  
 RL EMBO J. 6:3673-3677(1987).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM B).  
 RC SPECIES-Human;  
 RX MEDLINE=8816549; PubMed=3162414;  
 RA Madisen L., Webb N.R., Rose T.M., Marguardt H., Ikeda T.,  
 RA Twadzik D.R., Seyedin S., Purchio A.F.;  
 RT "Transforming growth factor-beta 2: cDNA cloning and sequence  
 RT analysis.";  
 RL DNA 7:1-8(1988).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORMS A AND B).  
 RC SPECIES-Human;  
 RX MEDLINE=89090808; PubMed=2850146;  
 RA Webb N.R., Madisen L., Rose T.M., Purchio A.F.;  
 RT "Structural and sequence analysis of TGF-beta 2 cDNA clones predicts  
 RT two different precursor proteins produced by alternative mRNA  
 RT splicing.";  
 RL DNA 7:493-497(1988).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM A).  
 RC SPECIES-C.aethiops;  
 RX MEDLINE=88124824; PubMed=3277172;  
 RA Hanks S., Armour R., Baldwin J.H., Maldonado F., Spleess J.,  
 RA Holley R.W.;  
 RT "Amino acid sequence of the BSC-1 cell growth inhibitor (polyergin)  
 RT deduced from the nucleotide sequence of the cDNA.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:79-82(1988).

RN [5]  
 RP SEQUENCE OF 1-115 FROM N.A.  
 RC SPECIES-Human; TISSUE=Lung;  
 RX MEDLINE=92110032; PubMed=1764261;  
 RA Noma T., Glick A.B., Geiser A.G., O'Reilly M.A., Miller J.,  
 RA Roberts A.B., Sporn M.B.;  
 RT "Molecular cloning and structure of the human transforming growth  
 RT factor-beta 2 gene promoter.";  
 RN Growth Factors 4:247-255(1991).  
 RN [6]  
 RP SEQUENCE OF 303-414.  
 RC SPECIES-Human;  
 RX MEDLINE=87308213; PubMed=3476488;  
 RA Marguardt H., Liobin M.N., Ikeda T.;  
 RT "Complete amino acid sequence of human transforming growth factor  
 RT type beta 2.";  
 RL J. Biol. Chem. 262:12127-12131(1987).  
 RN [7]  
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).  
 RX MEDLINE=92355881; PubMed=1631557;  
 RA Daopin S., Pletz K.A., Ogawa Y., Davies D.R.;  
 RT "Crystal structure of transforming growth factor-beta 2: an unusual  
 RT fold for the superfamily.";  
 RL Science 257:369-373(1992).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
 RX MEDLINE=92350287; PubMed=1641027;  
 RA Schlunegger M.P., Gruetter M.G.;  
 RT "An unusual feature revealed by the crystal structure at 2.2-A  
 RT resolution of human transforming growth factor-beta 2.";  
 RL Nature 358:430-434(1992).  
 RN [9]  
 RP VARIANT HIS-91.  
 RX MEDLINE=2149167; PubMed=11528528;  
 RA Alansari A., Hajjar A.H., Bayat A., Eyre S., Carthy D., Ollier W.E.;  
 RT "Two novel polymorphisms in the human transforming growth factor beta  
 RT 2 gene.";  
 RL Genes Immun. 2:295-296(2001).  
 CC -1- FUNCTION: TGF-BETA 2 HAS SUPPRESSIVE EFFECTS ON INTERLEUKIN-2  
 CC DEPENDENT T-CELL GROWTH.  
 CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B; ARE  
 CC PRODUCED BY AN ALTERNATIVE SPLICING. ISOFORM B IS ENCODED BY A MINOR  
 CC 5.1 KB MRNA SPECIES PRESENT IN HUMAN AND SIMIAN CELLS.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
 CC  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC  
 CC -----  
 CC EMBL: Y00083; CAA68279.1; -;  
 CC EMBL: M19154; AAA50404.1; -;  
 CC EMBL: M19154; AAA50405.1; ALT\_SEQ.  
 CC EMBL: J03585; AAA33558.1; -;  
 CC EMBL: M87843; AAA61162.1; -;  
 CC PIR: S06216; S06216.  
 CC PIR: A29478; A29478.  
 CC PIR: A29478; A29478.  
 CC PIR: A34005; A34005.  
 CC PIR: A34005; A34005.  
 CC PDB: 1TEG; 3I-OCT-93.  
 CC PDB: 2TGT; 3I-TAN-94.  
 CC Genew; HGNC:11768; TGF2.  
 CC MIM: 190220; -;  
 CC InterPro: IPR002400; GF\_cysknob.  
 CC InterPro: IPR003911; TGF\_TGFB.  
 CC InterPro: IPR001839; TGFB.  
 CC InterPro: IPR001111; TGFB\_N.  
 CC Pfam: PF00019; TGF-beta; 1.

DR Pfam; PF00688; TGFb.propeptide; 1.  
 DR PRINTS; PR00438; GFCYSKNOT.  
 DR PRINTS; PR01423; TGFbeta.  
 DR PRODOM; PD000357; TGFb; 1.  
 DR SMART; SM00204; TGFb; 1.  
 DR PROSITE; PS00250; TGF\_BETA\_1; 1.  
 DR Growth factor; Mitogen; Glycoprotein; Signal; Alternative splicing;  
 RW 3D-structure.  
 FT SIGNAL 1 19  
 FT PROPEP 20 302  
 FT CHAIN 303 414  
 FT DISULFID 309 318  
 FT DISULFID 317 380  
 FT DISULFID 346 411  
 FT DISULFID 350 413  
 FT DISULFID 379 379  
 FT CARBOHYD 72 72  
 FT CARBOHYD 140 140  
 FT CARBOHYD 241 241  
 FT VARSPLIC 116 116  
 FT  
 FT VARIANT 91 91  
 FT  
 FT CONFLICT 32 32  
 FT HELIX 306 309  
 FT TURN 310 311  
 FT STRAND 316 316  
 FT STRAND 318 320  
 FT STRAND 323 325  
 FT STRAND 326 330  
 FT TURN 333 334  
 FT STRAND 335 337  
 FT STRAND 340 342  
 FT STRAND 345 347  
 FT STRAND 349 349  
 FT TURN 352 353  
 FT STRAND 356 356  
 FT HELIX 359 370  
 FT HELIX 372 374  
 FT STRAND 380 382  
 FT STRAND 385 394  
 FT TURN 395 396  
 FT STRAND 397 408  
 FT STRAND 411 413  
 FT  
 FT SEQUENCE 414 AA; 47747 MW; 7D9D569E0FA07D0 CRC64;  
 Query Match 15.98; Score 25; DB 1; Length 414;  
 Best Local Similarity 30.88; Pred. No. 7.1e+02;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 QY 17 PXXXXXXXXXXGXC 29  
 DB 338 PKGYNANFCAGAC 350

RT "Murine transforming growth factor-beta 2 cDNA sequence and  
 expression in adult tissues and embryos."  
 RL Mol. Endocrinol. 3:1108-1114(1989).  
 CC -1- FUNCTION: TGF-BETA 2 HAS SUPPRESSIVE EFFECTS ON INTERLEUKIN-2  
 CC DEPENDENT T-CELL GROWTH.  
 CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
 CC  
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 CC or send an email to [license@isb-slb.ch](mailto:license@isb-slb.ch)).  
 CC  
 DR EMBL; X57413; CAA00672.1; -.  
 DR PIR; A40148; WFSB2.  
 DR HSSP; P08112; 2TGI.  
 DR MGD; MGI:98726; TGFb2.  
 DR InterPro; IPR002400; GF\_cysknnot.  
 DR InterPro; IPR003911; TGF\_TGFb.  
 DR InterPro; IPR001839; TGFb.  
 DR InterPro; IPR001111; TGFb\_N.  
 DR Pfam; PF00019; TGF-beta; 1.  
 DR Pfam; PF00688; TGFb.propeptide; 1.  
 DR PRINTS; PR00438; GFCYSKNOT.  
 DR PRINTS; PR01423; TGFbeta.  
 DR PRODOM; PD000357; TGFb; 1.  
 DR SMART; SM00204; TGFb; 1.  
 DR PROSITE; PS00250; TGF\_BETA\_1; 1.  
 DR Growth factor; Mitogen; Glycoprotein; Signal.  
 FT SIGNAL 1 19  
 FT PROPEP 20 302  
 FT CHAIN 303 414  
 FT DISULFID 309 318  
 FT DISULFID 317 380  
 FT DISULFID 346 411  
 FT DISULFID 350 413  
 FT DISULFID 379 379  
 FT CARBOHYD 72 72  
 FT CARBOHYD 140 140  
 FT CARBOHYD 241 241  
 FT  
 FT SEQUENCE 414 AA; 47601 MW; 449BC6FA22087EB6 CRC64;  
 Query Match 15.98; Score 25; DB 1; Length 414;  
 Best Local Similarity 30.88; Pred. No. 7.1e+02;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 QY 17 PXXXXXXXXXXGXC 29  
 DB 338 PKGYNANFCAGAC 350

Search completed: March 27, 2003, 11:00:10  
 Job time : 26 secs





SO SEQUENCE 102 AA; 9749 MW; 8BFE5ABD6AE78857 CRC64;  
 Query Match 17.2%; Score 27; DB 11; Length 102;  
 Best Local Similarity 30.8%; Pred. No. 3.5e+02;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXKCXC 29  
 DB 27 PAVTSGECTGSC 39

RESULT 2  
 09Y754 PRELIMINARY; PRT; 549 AA.  
 AC 09Y754;  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)  
 DE Siderophore biosynthesis repressor SREA.  
 GN SREA.  
 OS Emericella nidulans (Aspergillus nidulans).  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 OC Eurotiiales; Trichocomaceae; Emericella.  
 OX NCBI\_TaxID=5072;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-99143116; PubMed-9988696;  
 RA Haas H., Zadra I., Scofield G., Angermayr K.;  
 RT "The Aspergillus nidulans GATA factor SREA is involved in regulation  
 RT of siderophore biosynthesis and control of iron uptake.";  
 RL J. Biol. Chem. 274:4613-4619(1999).  
 DR EMBL: AF095898; AAD25328.1;  
 DR HSP; P1679; IGFN;  
 DR InterPro: IPR000679; Znf\_GATA.  
 DR Pfam: PF00320; GATA. 2.  
 DR PRINTS: PR00619; GATAZNFINGER.  
 DR SMART: SM00401; ZNF\_GATA. 2.  
 DR PROSITE: PS00344; GATA\_ZN\_FINGER.1; 2.  
 DR PROSITE: PS50114; GATA\_ZN\_FINGER.2;  
 DR PROSITE: PS50114; GATA\_ZN\_FINGER.2;  
 SO SEQUENCE 549 AA; 58842 MW; 359DC02AEFD62E3 CRC64;

Query Match 17.2%; Score 27; DB 3; Length 549;  
 Best Local Similarity 30.8%; Pred. No. 8.2e+02;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXKCXC 29  
 DB 168 PAVTSGECTGSC 180

RESULT 3  
 080540 PRELIMINARY; PRT; 967 AA.  
 AC 080540;  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)  
 DE Fl439.26 protein.  
 GN Fl439.26.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. COLUMBIA;  
 RA Federle N.A., Palm C.J., Conway A.B., Kurtz D.B., Conway A.R.,  
 RA Au M., Araujo R., Buehler E., Dewar K., Feng J., Kim C., Li Y.,  
 RA Oji O., Osborne B.J., Shin P., Sun H., Tortum M., Vysotskaia V.S.,  
 RA Yu G., Ecker J., Theologis A., Davis R.W.;  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

DR EMBL: AC003970; AAC33218.1; -.  
 DR HSP; P24941; IHCL.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR Pfam: PF00069; pkinase.1.  
 DR ProDom: PD000001; Euk\_pkinase.1.  
 DR SMART: SM00220; S\_TKc. 1.  
 DR PROSITE: PS0107; PROTEIN\_KINASE\_ATP; UNKNOWN\_1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM. 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST. 1.  
 DR AMP-binding; Serine/threonine-protein kinase; Transferase.  
 SO SEQUENCE 967 AA; 108177 MW; 6EB7F336C51289 CRC64;

Query Match 17.2%; Score 27; DB 10; Length 967;  
 Best Local Similarity 30.8%; Pred. No. 1.1e+03;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXKCXC 29  
 DB 726 P0ETSTRCTGSC 738

RESULT 4  
 042306 PRELIMINARY; PRT; 87 AA.  
 AC 042306;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)  
 DE Transforming growth factor beta (Fragment).  
 OS Carassius auratus (Goldfish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Carassius.  
 OX NCBI\_TaxID=7957;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=MACROPHAGE;  
 RA Daniels G.D., Belosevic M., Secombes C.J.;  
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: IS LIKELY TO BE AN IMPORTANT CYTOKINE REGULATING IMMUNE  
 CC RESPONSE. MAY ALSO HAVE A ROLE IN OTHER PHYSIOLOGICAL SYSTEMS.  
 CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
 DR EMBL: A001040; CAA04494.1; -.  
 DR HSP; P01137; IKLA.  
 DR InterPro: IPR001839; TGF.  
 DR Pfam: PF00019; TGF-beta. 1.  
 DR ProDom: PD000357; TGF. 1.  
 DR SMART: SM00204; TGF. 1.  
 DR PROSITE: PS00250; TGF\_BETA.1; 1.  
 DR Growth factor; Mitogen; Glycoprotein.  
 FT NON\_TER 1  
 FT CHAIN 1  
 FT DISULFID <1> 87  
 FT DISULFID 22 87  
 FT DISULFID 55 87  
 FT NON\_TER 87 87  
 SO SEQUENCE 87 AA; 10007 MW; 525465C4E8A70771 CRC64;

Query Match 16.6%; Score 26; DB 13; Length 87;  
 Best Local Similarity 30.8%; Pred. No. 4.7e+02;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXKCXC 29  
 DB 14 PGGYANYCTGSC 26

RESULT 5  
 0924A9 PRELIMINARY; PRT; 230 AA.  
 AC 0924A9;  
 DT 01-MAY-1999 (TREMBLrel. 10, Created)

01-MAY-1999 (TREMBlrel. 10, last sequence update)  
 01-DEC-2001 (TREMBlrel. 19, last annotation update)  
 DE Tram protein.  
 GN Shigella sonnei.  
 OS Plasmid Colib-P9.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Shigella.  
 OX NCBI\_TaxID=624;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-P9; Mizobuchi K.;  
 RA "Organization and diversification of plasmid genomes: complete  
 RT nucleotide sequence of the Colib-P9 genome."  
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB021078; BAA75159.1;  
 KW Plasmid.  
 SQ SEQUENCE 230 AA; 25561 MW; FEE050B13F09FA1 CRC64;  
 Query Match 16.6%; Score 26; DB 2; Length 230;  
 Best Local Similarity 30.8%; Pred. No. 7.8e+02;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

0Y 17 PXXXXXXCXGXC 29  
 DB 38 PALIKALCTGTC 50

RESULT 6  
 09R2H2 PRELIMINARY; PRT; 230 AA.  
 AC 09R2H2;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)  
 DE Tram protein.  
 GN Salmonella typhimurium.  
 OS Salmonella typhimurium.  
 OC Plasmid R64.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Salmonella.  
 OX NCBI\_TaxID=602;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-DRD-11;  
 RA Komano T., Narehara K., Yoshida T., Furuya N.;  
 RT "The transfer region of IncII plasmid R64: similarities between R64  
 RT tra genes and Legionella lsm/dot genes."  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-DRD-11;  
 RX MEDLINE=92011438; PubMed=1917882;  
 RA Furuya N., Komano T.;  
 RT "Determination of the nick site at oriT of IncII plasmid R64: global  
 RT similarity of oriT structures of IncII and IncP plasmids."  
 RL J. Bacteriol. 173:6612-6617(1991).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-DRD-11;  
 RX MEDLINE=98053841; PubMed=9393692;  
 RA Furuya N., Komano T.;  
 RT "Mutational analysis of the R64 oriT region: requirement for precise  
 RT location of the Nika-binding sequence."  
 RL J. Bacteriol. 179:7291-7297(1997).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-DRD-11;  
 RX MEDLINE=98268996; PubMed=9603870;  
 RA Yoshida T., Furuya N., Ishikura M., Isobe T., Haino-Fukushima K.,  
 RA Ogawa T., Komano T.;  
 RT "Purification and characterization of thin pill of IncII plasmids

Colib-P9 and R64: formation of PiliV-specific cell aggregates by type  
 IV Pili."  
 RL J. Bacteriol. 180:2842-2848(1998).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-DRD-11;  
 RX MEDLINE=94132048; PubMed=8300611;  
 RA Pansegrau W., Schröder W., Lanka E.;  
 RT "Concerted action of three distinct domains in the DNA cleaving-  
 RT joining reaction catalyzed by relaxase (TraI) of conjugative plasmid  
 RP4."  
 RL J. Biol. Chem. 269:2782-2789(1994).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-DRD-11;  
 RX MEDLINE=94285211; PubMed=8014987;  
 RA Pansegrau W., Lanka E., Barth P.T., Figurski D.H., Guiney D.G.,  
 RA Haas D., Helinski D.R., Schwab H., Stansich V.A., Thomas C.M.;  
 RT "Complete nucleotide sequence of Birmingham IncP-alpha plasmids:  
 RT compilation and comparative analysis."  
 RL J. Mol. Biol. 239:623-663(1994).  
 DR EMBL; AB027308; BAA78001.1;  
 KW Plasmid.  
 SQ SEQUENCE 230 AA; 25560 MW; F43394751D05AB90 CRC64;

Query Match 16.6%; Score 26; DB 2; Length 230;  
 Best Local Similarity 30.8%; Pred. No. 7.8e+02;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

0Y 17 PXXXXXXCXGXC 29  
 DB 38 PALIKALCTGTC 50

RESULT 7  
 09SDK7 PRELIMINARY; PRT; 240 AA.  
 AC 09SDK7;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)  
 DE Hypothetical protein.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; Oryza.  
 OX NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CV. NIPPONBARE;  
 RA Sasaki T., Matsumoto T., Yamamoto K.;  
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC  
 RT clone:P0705D01."  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF000492; BAA84609.1;  
 KW Hypothetical protein.  
 SQ SEQUENCE 240 AA; 26333 MW; E67BC59CB18F9BD CRC64;

Query Match 16.6%; Score 26; DB 10; Length 240;  
 Best Local Similarity 30.8%; Pred. No. 8e+02;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

0Y 17 PXXXXXXCXGXC 29  
 DB 146 PAAAAAFCGCGPC 158

RESULT 8  
 09H7T3 PRELIMINARY; PRT; 257 AA.  
 AC 09H7T3;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, last sequence update)

DT 01-MAR-2001 (TREMBlrel. 16, last annotation update)  
 DE CDNA FLJ14280 fls, clone PLACE1005584, weakly similar to trans-acting  
 OS Homo sapiens (human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA TISSUE-PLACENTA;  
 RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
 RA Nishikawa T., Nagai K., Sugano S., Shitatori A., Sudo H.,  
 RA Wagatsuma M., Hosokawa T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,  
 RA Takahashi M., Chiba Y., Ishida S., Murakami K., Ono Y., Takiguchi S.,  
 RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,  
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Masuho Y.,  
 RA Niimura K., Iwaguchi T.;  
 RT "NCBI human cDNA sequencing project."  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AK024342; BAB1482.1;  
 SQ SEQUENCE 257 AA; 26269 MW; B914A57EA54DF18 CRC64;

Query Match 16.6%; Score 26; DB 4; Length 257;  
 Best Local Similarity 30.8%; Pred. No. 8.3e+02;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 17 PXXXXXXCXGXC 29  
 DB 179 PLCTSTSCAGSC 191

RESULT 9  
 ID 017764 PRELIMINARY; PRT; 278 AA.  
 AC 017764;  
 DT 01-JAN-1998 (TREMBlrel. 05, Created)  
 DT 01-JAN-1998 (TREMBlrel. 05, last sequence update)  
 DE 01-DEC-2001 (TREMBlrel. 19, last annotation update)  
 GN F01G10.6 protein.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;  
 OC Rhabditidae; Pelodierinae; Caenorhabditis.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hemphry C.;  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 RP [2]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-99069613; PubMed-9851916;  
 RA none;  
 RT "Genome sequence of the nematode C. elegans: A platform for  
 RT investigating biology."  
 RL Science 282:2012-2018(1998).  
 DR EMBL: Z81055; CAB02894.1;  
 SQ SEQUENCE 278 AA; 30945 MW; 9C5B0F9F3C88577A CRC64;

Query Match 16.6%; Score 26; DB 5; Length 278;  
 Best Local Similarity 30.8%; Pred. No. 8.6e+02;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 17 PXXXXXXCXGXC 29  
 DB 59 PSMTFAESGSGPC 71

RESULT 10  
 ID 018027 PRELIMINARY; PRT; 347 AA.  
 AC 018027;  
 DT 01-JAN-1998 (TREMBlrel. 05, Created)  
 DT 01-JAN-1998 (TREMBlrel. 05, last sequence update)

DT 01-MAR-2002 (TREMBlrel. 20, last annotation update)  
 DE T05E12.1 protein.  
 GN T05E12.1  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;  
 OC Rhabditidae; Pelodierinae; Caenorhabditis.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA McMurray A.A.;  
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 RP [2]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-99069613; PubMed-9851916;  
 RA none;  
 RT "Genome sequence of the nematode C. elegans: A platform for  
 RT investigating biology."  
 RL Science 282:2012-2018(1998).  
 DR EMBL: Z81585; CAB04681.1;  
 DR InterPro: IPR003002; TrmChemol.  
 DR Pfam: PF01461; Trm\_4; 1.  
 SQ SEQUENCE 347 AA; 39762 MW; B97BA2961988A85A CRC64;

Query Match 16.6%; Score 26; DB 5; Length 347;  
 Best Local Similarity 30.8%; Pred. No. 9.6e+02;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 17 PXXXXXXCXGXC 29  
 DB 87 PLATTSRGFLC 99

RESULT 11  
 ID 08R209 PRELIMINARY; PRT; 349 AA.  
 AC 08R209;  
 DT 01-JUN-2002 (TREMBlrel. 21, Created)  
 DT 01-JUN-2002 (TREMBlrel. 21, last sequence update)  
 DE 01-JUN-2002 (TREMBlrel. 21, last annotation update)  
 GN Mus musculus (Mouse).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA TISSUE-COLON;  
 RA Strausberg R.;  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC022669; AAH22669.1;  
 KW Hypothetical protein.  
 FT NON\_TER  
 SQ SEQUENCE 349 AA; 39115 MW; D361C92578686F63 CRC64;

Query Match 16.6%; Score 26; DB 11; Length 349;  
 Best Local Similarity 30.8%; Pred. No. 9.7e+02;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 17 PXXXXXXCXGXC 29  
 DB 268 PKSPDAYCAGAC 280

RESULT 12  
 ID 09DFC6 PRELIMINARY; PRT; 366 AA.  
 AC 09DFC6;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)  
 DE TGF-beta family member lefty-A.  
 OS Xenopus laevis (African clawed frog).



OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20341055; PubMed=10882517;  
 RA Brantford W.W., Essner J.J., Yost H.J.;  
 RT "Regulation of gut and heart left-right asymmetry by context-dependent  
 interactions between Xenopus lefty and BMP4 signaling.";  
 RL Dev. Biol. 223:291-306(2000).  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
 DR EMBL: AF283562; AAC10034.1; -.  
 DR HSSP: P18075; IBM.  
 DR InterPro: IPR001839; TGFb.  
 DR InterPro: IPR001111; TGFb\_N.  
 DR Pfam: PF000019; TGF-beta; 1.  
 DR Pfam: PF00688; TGFb\_propeptide; 1.  
 DR ProDom: PD000357; TGFb; 1.  
 DR SMART: SM00204; TGFb; 1.  
 DR PROSITE: PS00250; TGF\_BETA\_1; 1.  
 KW Glycoprotein.  
 SQ SEQUENCE 366 AA; 41434 MW; E65CEC306F4B5ED5 CRC64;  
 Query Match 16.6%; Score 26; DB 13; Length 366;  
 Best Local Similarity 30.8%; Pred. No. 9.9e+02;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 OY 17 PXXXXXXCXGXC 29  
 DB 293 PAGYNAFRCAGSC 305  
 RESULT 13  
 OQ9D36 PRELIMINARY; PRT; 367 AA.  
 AC O9D36;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)  
 DE Xantivin (Lefty-related factor Xatv).  
 GN XANTIVIN.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=11091069;  
 RA Tanegashima K., Yokota C., Takahashi S., Asashima M.;  
 RT "Expression cloning of Xantivin, a Xenopus lefty/antiyvin-related gene,  
 involved in the regulation of activin signaling during mesoderm  
 induction.";  
 RL Mech. Dev. 99:3-14(2000).  
 CC [2]  
 RN SEQUENCE FROM N.A.  
 RP Cheng A.M.S., Thisse B., Thisse C., Wright C.V.E.;  
 RA "The lefty-related factor Xatv acts as a feedback inhibitor of nodal  
 signaling in mesoderm induction and L-R axis development in Xenopus.";  
 RT development 0-0-0(2000)  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
 DR EMBL: AB038010; BAB12725.1; -.  
 DR EMBL: AF209744; AAG35771.1; -.  
 DR HSSP: P08112; 2TGI.  
 DR InterPro: IPR001839; TGFb.  
 DR InterPro: IPR001111; TGFb\_N.  
 DR Pfam: PF000019; TGF-beta; 1.  
 DR Pfam: PF00688; TGFb\_propeptide; 1.  
 DR ProDom: PD000357; TGFb; 1.  
 DR SMART: SM00204; TGFb; 1.  
 DR PROSITE: PS00250; TGF\_BETA\_1; 1.  
 KW Glycoprotein.

SQ SEQUENCE 367 AA; 41504 MW; DEAA90275BC8574A CRC64;  
 Query Match 16.6%; Score 26; DB 13; Length 367;  
 Best Local Similarity 30.8%; Pred. No. 9.9e+02;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 OY 17 PXXXXXXCXGXC 29  
 DB 293 PAGYNAFRCAGSC 305  
 RESULT 14  
 OQ9D36 PRELIMINARY; PRT; 367 AA.  
 AC O9D36;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)  
 DE TGF-beta family member lefty-B.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20341055; PubMed=10882517;  
 RA Brantford W.W., Essner J.J., Yost H.J.;  
 RT "Regulation of gut and heart left-right asymmetry by context-dependent  
 interactions between Xenopus lefty and BMP4 signaling.";  
 RL Dev. Biol. 223:291-306(2000).  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
 DR EMBL: AF283563; AAC10035.1; -.  
 DR HSSP: P08112; 2TGI.  
 DR InterPro: IPR001839; TGFb.  
 DR InterPro: IPR001111; TGFb\_N.  
 DR Pfam: PF000019; TGF-beta; 1.  
 DR Pfam: PF00688; TGFb\_propeptide; 1.  
 DR ProDom: PD000357; TGFb; 1.  
 DR SMART: SM00204; TGFb; 1.  
 DR PROSITE: PS00250; TGF\_BETA\_1; 1.  
 KW Glycoprotein.  
 SQ SEQUENCE 367 AA; 41604 MW; DBA7E85752B7FB3A CRC64;  
 Query Match 16.6%; Score 26; DB 13; Length 367;  
 Best Local Similarity 30.8%; Pred. No. 9.9e+02;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 OY 17 PXXXXXXCXGXC 29  
 DB 293 PAGYNAFRCAGSC 305  
 RESULT 15  
 OQ9PTQ2 PRELIMINARY; PRT; 376 AA.  
 AC O9PTQ2;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)  
 DE Transforming growth factor beta precursor.  
 OS Cyprinus carpio (Common carp).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Cyprinus.  
 OX NCBI\_TaxID=7962;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Yin Z., Kuang J.;  
 RT "Molecular cloning of carp transforming growth factor beta 1.";  
 RL submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: IS LIKELY TO BE AN IMPORTANT CYTOKINE REGULATING IMMUNE  
 RESPONSE. MAY ALSO HAVE A ROLE IN OTHER PHYSIOLOGICAL SYSTEMS.

CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).  
 CC EMBL: AFI36947; AAF22573.1; -.  
 DR HSSP: P01137; IKLA.  
 DR InterPro: IPR001839; TGF.  
 DR InterPro: IPR001111; TGF\_N.  
 DR Pfam: PF00688; TGF\_beta; 1.  
 DR ProDom: PD000357; TGF; 1.  
 DR SMART: SM00204; TGF; 1.  
 DR PROSITE: PS00250; TGF\_BETA\_1; 1.  
 KW Growth factor: Mitogen; Glycoprotein; Signal.  
 FT SIGNAL 1 22 POTENTIAL.  
 FT PROPEP 23 264  
 FT CHAIN 265 376 TRANSFORMING GROWTH FACTOR BETA.  
 FT DISULFID 272 280 BY SIMILARITY.  
 FT DISULFID 308 373 BY SIMILARITY.  
 FT DISULFID 312 375 BY SIMILARITY.  
 FT DISULFID 341 341 INTERCHAIN (BY SIMILARITY).  
 FT CARBOHYD 76 76 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 125 125 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 167 167 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT SITE 230 232 CELL ATTACHMENT SITE (POTENTIAL).  
 SQ SEQUENCE 376 AA; 43329 MM; 7F7FC4DA58B69681 CRC64;

Query Match 16.6%; Score 26; DB 13; Length 376;  
 Best Local Similarity 30.8%; Pred. No. 1e+03;  
 Matches 4; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 17 PXXXXXXCXGXC 29  
 DB 300 PSGYANTCTGSC 312

Search completed: March 27, 2003, 11:01:43  
 Job time : 87 secs